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125082

From: Hamud, Fozia
Sent: Tuesday, December 27, 2005 12:34 PM
To: STIC-Biotech/ChemLib
Subject: sequence search 10/691,923

Hello,
Kindly search SEQ ID NO:34 of 10/691,923 against commercial and interference data bases. Thank you.

FOZIA HAMUD
PATENT EXAMINER
ART UNIT 1647
ROOM:REM 4D64
MAIL BOX: REM 4C70

CRFF

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: _____
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 29, 2005, 13:46:42 ; Search time 227 Seconds
(without alignments)
565.666 Million cell updates/sec

Title: US-10-691-923-34

Perfect score: 955

Sequence: 1 MGVPVTSKPTTGGKCHIGR.....LKTVADGNLSLRTSTHPST 182

Scoring table: BLOSUM62

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	945	99.0	200	1 IL29 HUMAN	Q81u54 homo sapien
2	667.5	69.9	200	1 IL28B HUMAN	Q81z19 homo sapien
3	653.5	68.4	200	1 IL28A HUMAN	Q81zj0 homo sapien
4	477	49.9	193	2 Q4VK74 MOUSE	Q4vk74 mus musculus
5	463	48.5	193	2 Q4VK73 MOUSE	Q4vk73 mus musculus
6	458	48.0	193	1 IL28 MOUSE	Q8cgk6 mus musculus
7	97.5	10.2	692	1 PKK ACIBA	Q9x4m8 acinetobact
8	89.5	9.4	914	2 Q4ZV84 PSESY	Q4zv84 pseudomonas
9	89	9.3	296	2 Q8G5G0 BIFLO	Q8g5g0 bifidobacte
10	89	9.3	458	2 Q8DJLO STNEL	Q8dj10 synecococc
11	88.5	9.3	313	2 Q75BW8 ASHGO	Q75bw8 ashbya goss
12	87.5	9.2	953	2 Q6FCX8 ACTAD	Q6fcx8 acinetobact
13	87	9.1	479	2 Q7QZJ8 GIALA	Q7qzj8 giardia lam
14	86.5	9.1	967	2 Q5B9M4 ASPERILLUS	Q5b9m4 aspergillus
15	86	9.0	333	2 Q58D46 BOVIN	Q58d46 bos taurus
16	86	9.0	528	2 Q4KB02 PSEF5	Q4kb02 pseudomonas
17	86	9.0	567	2 Q5EA80 BOVIN	Q5ea80 bos taurus
18	85.5	9.0	574	2 Q52GV5 MAGGR	Q52gv5 magnaporthe
19	85.5	9.0	2173	2 Q4C895 LEIMA	Q4c895 leishmania
20	85	8.9	673	2 Q57P25 SALCH	Q57p25 salmonella
21	85	8.9	975	2 Q4C6B0 LEIMA	Q4c6b0 leishmania
22	84.5	8.8	371	2 Q6SP70 9RETR	Q6sp70 small rumin
23	84.5	8.8	455	2 Q5SG79 ARATH	Q5sg79 arabidopsis
24	84.5	8.8	881	2 Q6OAC8 METCA	Q6oac8 methylococc
25	84.5	8.8	918	2 Q884J3 PSESM	Q884j3 pseudomonas
26	84.5	8.8	1122	2 Q8J4V1 9RETR	Q8j4v1 viana/maedi
27	84.5	8.8	1799	1 DCKG HUMAN	Q8nf50 homo sapien
28	84.5	8.8	2032	2 Q5JPJ1 HUMAN	Q5jpp1 homo sapien
29	84	8.8	204	2 Q88N24 PSEPK	Q88n24 pseudomonas
30	84	8.8	663	2 Q9NV65 HUMAN	Q9nv65 homo sapien
31	84	8.8	1379	2 Q7QEK5 ANOGA	Q7qek5 anopheles g

32 83.5 8.7 414 2 Q69TN3 ORYSA
33 83.5 8.7 499 2 Q4FBH3 ECOLI
34 83.5 8.7 597 2 Q7ULZ9 XROBA
35 83.5 8.7 716 2 Q6C489 YARLI
36 83.5 8.7 1470 2 Q8CHD4 MOUSE
37 83 8.7 567 1 PGTA HUMAN
38 83 8.7 567 2 Q6PHF7 HUMAN
39 83 8.7 567 2 Q5NVK5 PONPY
40 83 8.7 739 2 Q8BI71 MOUSE
41 83 8.7 889 2 Q8DLX6 STNEL
42 82.5 8.6 1443 2 Q4T8K2 TETNG
43 82.5 8.6 3317 2 Q9RAH2 NOSO
44 82 8.6 315 1 SPY2 MOUSE
45 82 8.6 899 1 PRP6 YEAST

ALIGNMENTS

RESULT 1
IL29 HUMAN
ID IL29 HUMAN STANDARD; PRT; 200 AA.
AC Q81U54;
DT 01-FEB-2005 (Rel. 46, Created)
DT 01-FEB-2005 (Rel. 46, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Interleukin 29 precursor (IL-29) (Interferon lambda-1) (IFN-lambda-1)
DE (Cytokine ZCYTO21).
GN Name=IL29; Synonyms=IFNL1, ZCYTO21;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=12469119; DOI=10.1038/ni873;
RA Sheppard P., Kindvogel W., Xu W., Henderson K., Schlutsmeyer S.,
RA Whitmore T.E., Kuestner R., Garrigue U., Birks C., Roraback J.,
RA Ostrander C., Dong D., Shin J., Presnell S., Fox B., Haldeman B.,
RA Cooper E., Taft D., Gilbert T., Grant F.J., Tackett M., Krivan W.,
RA McKnight G., Clegg C., Foster D., Klucher K.M.;
RA "IL-28, IL-29 and their class II cytokine receptor IL-28R.";
RL Nat. Immunol. 4:63-68(2003).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=12483210; DOI=10.1038/ni875;
RA Kotenko S.V., Gallagher G., Baurin V.V., Lewis-Antes A., Shen M.,
RA Shah N.K., Langer J.A., Sheikh F., Dickensheets H., Donnelly R.P.;
RA "IFN-lambdas mediate antiviral protection through a distinct class II
cytokine receptor complex.";
RL Nat. Immunol. 4:69-77(2003).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan B., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences".
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 CC -1- FUNCTION: Cytokine with immunomodulatory activity. May play a role
 CC in antiviral immunity. Up-regulates MHC class I antigen
 CC expression. Ligand for the heterodimeric class II cytokine
 CC receptor composed of IL10RB and IL28RA. The ligand/receptor
 CC complex seems to signal through the Jak-STAT pathway.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- INDUCTION: By viral infections or double stranded RNA.
 CC -1- SIMILARITY: Belongs to the IL-28/IL-29 family.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC
 CC EMBL; AY129150; AAN28265.1; -; mRNA.
 CC EMBL; AY184372; AAN86125.1; -; mRNA.
 CC EMBL; AY336716; AAR24509.1; -; mRNA.
 CC EMBL; BC074985; AAH74985.1; -; mRNA.
 CC Ensembl; ENSG00000182393; Homo sapiens.
 CC HGNC; HGNC:18363; IL29.
 CC MIM; 607403; -.
 CC Antiviral defense; Cytokine; Glycoprotein; Signal.
 FT SIGNAL 1 19 Potential.
 FT CHAIN 20 200 Interleukin 29.
 FT CARBOHYD 65 65 N-linked (GlcNAc...) (Potential).
 FT SEQUENCE 200 AA; 21898 MW; D4433B9462DCB4A1 CRC64;
 Query Match 99.0%; Score 945; DB 1; Length 200;
 Best Local Similarity 99.4%; Pred. No. 2.4e-78;
 Matches 180; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 GPVPTSKPTTTGKCHGRFKSLSPQELASPKKARDALAEESLKLKWNSSCPVPFGNWL 61
 DB 20 GPVPTSKPTTTGKCHGRFKSLSPQELASPKKARDALAEESLKLKWNSSCPVPFGNWL 79
 QY 62 RLQVRRPVALEAEALTLKVLAAAGPALEDVLDQPLHTLHLHLSQLQACIQPTAG 121
 DB 80 RLQVRRPVALEAEALTLKVLAAAGPALEDVLDQPLHTLHLHLSQLQACIQPTAG 139
 QY 122 PRPRGRLLHHLRLQEAAPKESACLEASVTFNLLTRDLTKYVADGNLSLRTSTHPES 181
 DB 140 PRPRGRLLHHLRLQEAAPKESACLEASVTFNLLTRDLTKYVADGNLSLRTSTHPES 199
 QY 182 T 182
 DB 200 T 200
 RESULT 2
 ID IL28B HUMAN STANDARD; PRT; 200 AA.
 AC Q81Z19; O6VNS56; Q72AJ3; Q81WL6;
 DT 01-FEB-2005 (Rel. 46, Created)
 DT 01-FEB-2005 (Rel. 46, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Interleukin 28B precursor (IL-28C) (Interferon lambda-3)
 DE (IFN-lambda-3) (Interferon lambda-4) (IFN-lambda-4) (Cytokine
 DE ZCYTO22).
 GN Name=IL28B; Synonyms=IFNL3, IFNL4, IL28C, ZCYTO22;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.

NCBI_TaxID=9606;
 [1]
 NUCLEOTIDE SEQUENCE, FUNCTION, AND INDUCTION.
 RX PubMed=12469119; DOI=10.1038/nr1873;
 RA Sheppard P., Kindsvogel W., Xu W., Henderson K., Schlutemeyer S.,
 RA Whitmore T.E., Kuestner R., Garrigues U., Birks C., Roraback J.,
 RA Ostrander C., Dong D., Shin J., Prensell S., Fox B., Haldeman B.,
 RA Cooper E., Taft D., Gilbert T., Grant P.J., Tackett M., Krivan W.,
 RA McKnight G., Clegg C., Foster D., Klucher K.M.;
 RT "IL-28, IL-29 and their class II cytokine receptor IL-28R".
 RL Nat. Immunol. 4:63-68(2003).
 [2]
 NUCLEOTIDE SEQUENCE OF 5-200, FUNCTION, SUBCELLULAR LOCATION, AND
 INDUCTION.
 RX PubMed=12483210; DOI=10.1038/nr1875;
 RA Kotenko S.V., Gallagher G., Bauzin V.V., Lewis-Antes A., Shen M.,
 RA Shah N.K., Langer J.A., Sheikh F., Dickensheets H., Donnelly R.P.;
 RT "IFN-lambda mediate antiviral protection through a distinct class II
 RT cytokine receptor complex".
 RL Nat. Immunol. 4:69-77(2003).
 [3]
 NUCLEOTIDE SEQUENCE OF 4-200.
 RA Li M., He S.;
 RT "Construction of mammalian cell expression vector of human interleukin
 RT IL-29, IL-28A, IL-28B and IL-28C gene from activated peripheral blood
 RT mononuclear cell and analysis of its sequence".
 RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Cytokine with immunomodulatory activity. May play a role
 CC in antiviral immunity. Up-regulates MHC class I antigen
 CC expression. Ligand for the heterodimeric class II cytokine
 CC receptor composed of IL10RB and IL28RA. The ligand/receptor
 CC complex seems to signal through the Jak-STAT pathway.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- INDUCTION: By viral infections or double stranded RNA.
 CC -1- SIMILARITY: Belongs to the IL-28/IL-29 family.
 CC -1- CAUTION: It is uncertain whether Met-1 or Met-5 is the initiator.
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC
 CC EMBL; AY129149; AAN28264.1; -; mRNA.
 CC EMBL; AY184374; AAN86127.1; -; mRNA.
 CC EMBL; AY336714; AAR24509.1; ALT_INIT; mRNA.
 CC EMBL; AY336717; AAO01561.1; ALT_INIT; mRNA.
 CC Ensembl; ENSG00000197110; Homo sapiens.
 CC HGNC; HGNC:18365; IL28B.
 CC MIM; 607402; -.
 CC Antiviral defense; Cytokine; Signal.
 FT SIGNAL 1 25 Potential.
 FT CHAIN 26 200 Interleukin 28B.
 FT CONFLICT 74 74 K -> R (in Ref. 3; AAO01561).
 FT CONFLICT 112 112 T -> S (in Ref. 2).
 FT CONFLICT 124 124 D -> G (in Ref. 3; AAO01561).
 FT CONFLICT 159 159 L -> P (in Ref. 3; AAO01561).
 FT CONFLICT 160 160 H -> Y (in Ref. 2).
 FT SEQUENCE 200 AA; 22194 MW; 4DD71C5DAC6D7E66 CRC64;
 Query Match 69.9%; Score 667.5; DB 1; Length 200;
 Best Local Similarity 76.6%; Pred. No. 6.3e-53;
 Matches 134; Conservative 11; Mismatches 25; Indels 5; Gaps 2;
 QY 2 GPVPTSK---PTTGTGKCHGRFKSLSPQELASPKKARDALAEESLKLKWNSSCPVPFGN 58
 DB 24 GAVPVARLRGALPDARGCHTAQFKSLSPQELQAFKRDALAEESLLKDKCKRSLRPT 83
 QY 59 WDLRLQVRRPVALEAEALTLKVLAAAGPALEDVLDQPLHTLHLHLSQLQACIQP 116
 DB 84 WDLRLQVRRPVALEAEALTLKVLAAAGPALEDVLDQPLHTLHLHLSQLQACIQP 143
 QY 117 QPTAGPRGRLLHHLRLQEAAPKESACLEASVTFNLLTRDLTKYVADGNL 171


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DE Interferon-lambda3.
GN Name=1128; Synonyms=Ifnl3;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=129/Sv;
RX PubMed=15120645; DOI=10.1016/j.intimp.2004.01.003;
RA Kotenko S.V., Langer J.A.;
RT "Full house: 12 receptors for 27 cytokines.";
RL Int. Immunopharmacol. 4:593-608(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=129/Sv;
RX PubMed=15914836; DOI=10.1099/vir.0.80904-0;
RA Bartlett N.W., Buttigieg K., Kotenko S.V., Smith G.L.;
RT "Murine interferon lambdas (type III interferons) exhibit potent
RT antiviral activity in vivo in a poxvirus infection model.";
RL J. Gen. Virol. 86:1589-1596(2005).
DR EMBL; AY869696; AAX58715.1; -; mRNA.
DR MGI; MGI:2450574; I128.
SQ SEQUENCE 193 AA; 21690 MW; 9CBBA23911F9B332 CRC64;

Query Match 48.5%; Score 463; DB 2; Length 193;
Best Local Similarity 58.8%; Pred. No. 3.3e-34;
Matches 100; Conservative 19; Mismatches 49; Indels 2; Gaps 2;

QY 3 PVP-TSKPTTTGKGCHGRFSLSPQELASPKKARDALAEESLKLKNWSCSSPVFPNGNDL 61
DB 21 PVPRATRLPVEAKDCHIAQFKSLSPKELQAFKKAIAEKLEKXDRCSHLISRAWDL 80

QY 62 RLLQVRPVALEAEALTLKVLAAAGPALEDVLDQPLHLTHLSLQLOACIQPQTAG 121
DB 81 KQLQVQRPKALQAEVALTLKWNINDSALTTLGQPLHLTHLSLQLOCTQLQATAE 140

QY 122 PRPRG-RLHHLWLRLQAPKESAGCLEASVTNLFRLTLRLDKLVADGN 170
DB 141 PKPPRRRLRWLRLQEAQSKETPGCLEDVTSNLFQLLRLDLKCVASGD 190

RESULT 6
IL28_MOUSE
ID IL28_MOUSE STANDARD; PRT; 193 AA.
AC Q8CGK6;
DT 01-FEB-2005 (Rel. 46, Created)
DT 01-FEB-2005 (Rel. 46, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Interleukin 28 precursor (interferon lambda) (IFN-lambda).
GN Name=1128;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6;
RX PubMed=12483210; DOI=10.1038/n1875;
RA Kotenko S.V., Gallagher G., Baurin V.V., Lewis-Antes A., Shen M.,
RA Shah N.K., Langer J.A., Sheikh F., Dickensheets H., Donnelly R.P.;
RT "IFN-lambdas mediate antiviral protection through a distinct class II
RT cytokine receptor complex.";
RL Nat. Immunol. 4:69-77(2003).
CC -!- FUNCTION: Cytokine with immunomodulatory activity. May play a role
CC in antiviral immunity. Up-regulates MHC class I antigen
CC expression. Ligand for the heterodimeric class II cytokine
CC receptor composed of IL10RB and IL28RA. The ligand/receptor
CC complex seems to signal through the Jak-STAT pathway (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).

```

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CC -!- SIMILARITY: Belongs to the IL-28/IL-29 family.
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; AY184375; AAN86128.1; -; mRNA.
CC DR EMBL; ENSMUSG0000060747; Mus musculus.
CC MGI; MGI:2450574; I128.
CC KW Antiviral defense; Cytokine; Signal.
CC FT SIGNAL 1 19
CC CHAIN 20 193 Interleukin 28.
CC SQ SEQUENCE 193 AA; 21664 MW; 357A00AACAA9BC61 CRC64;

Query Match 48.0%; Score 458; DB 1; Length 193;
Best Local Similarity 59.2%; Pred. No. 9.4e-34;
Matches 99; Conservative 19; Mismatches 50; Indels 2; Gaps 2;

QY 3 PVP-TSKPTTTGKGCHGRFSLSPQELASPKKARDALAEESLKLKNWSCSSPVFPNGNDL 61
DB 21 PVPRATRLPVEAKDCHIAQFKSLSPKELQAFKKAIAEKLEKXDRCSHLISRAWDL 80

QY 62 RLLQVRPVALEAEALTLKVLAAAGPALEDVLDQPLHLTHLSLQLOACIQPQTAG 121
DB 81 KQLQVQRPKALQAEVALTLKWNINDSALTTLGQPLHLTHLSLQLOCTQLQATAE 140

QY 122 PRPRG-RLHHLWLRLQAPKESAGCLEASVTNLFRLTLRLDKLVADGN 170
DB 141 PKPPRRRLRWLRLQEAQSKETPGCLEDVTSNLFQLLRLDLKCVASGD 190

RESULT 7
PPK_ACIBA
ID PPK_ACIBA STANDARD; PRT; 692 AA.
AC Q9X4M8;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Polychosphate kinase (EC 2.7.4.1) (Polychosphoric acid kinase) (ATP-
DE polychosphate phosphotransferase).
GN Name=ppk;
OS Acinetobacter baumannii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Moraxellaceae; Acinetobacter.
OX NCBI_TaxID=470;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=252;
RX MEDLINE=20005607; PubMed=10537215;
RA Gavigan J.A., Marshall L.M., Dobson A.D.W.;
RT "Regulation of polychosphate kinase gene expression in Acinetobacter
RT baumannii 252.";
RL Microbiology 145:2931-2937(1999).
CC -!- FUNCTION: Catalyzes the reversible transfer of the terminal
CC phosphate of ATP to form a long-chain polychosphate (polyP).
CC -!- CATALYTIC ACTIVITY: ATP + (phosphate) (n) = ADP + (phosphate) (n+1).
CC -!- PTM: An intermediate of this reaction is the autophosphorylated
CC residues through a N-P bond (By similarity).
CC -!- SIMILARITY: Belongs to the polychosphate kinase family.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; AF116175; AAD28429.1; -; Genomic_DNA.
CC HAWAP; MF_00347; -; 1.
CC InterPro; IPR003414; PP_kinase.
CC Pfam; PF02503; PP_kinase; 1.

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KW Phosphorylation; Transferase.
FT ACT_SITE 443 443 Phosphohistidine intermediate (By similarity).
FT ACT_SITE 462 462 Phosphohistidine intermediate (By similarity).
SQ SEQUENCE 692 AA; 78980 MW; C7EB001DF332920 CRC64;
Query Match 10.2%; Score 97.5; DB 1; Length 692;
Best Local Similarity 22.6%; Pred. No. 4.5;
Matches 42; Conservative 28; Mismatches 63; Indels 53; Gaps 8;
QY 24 LSPQELAS--FKKADALEESLKLKNSWSSVFFGNWDLRLQVRRPVAL-----E 74
Db 85 LSPQELHQSITAHAAERQOILN---EQIFP-----QLREGISFLRRGELTQ 132
QY 75 AELALTALKVLEAAAGPVEDVLDQLH-----TLHHLS-----QLQACIOPO 117
Db 133 AQSNVKKYFQEOVAPALPTISLDAHPFRLVKNLSNFIIVLEKDAFGROIDLVAP 192
QY 118 PTAGPR-----PRGRHLHWL-----HRLQAPKESAGCLEASVTNLFRLTRD 162
Db 193 PHSLPVRLVLPDELTEGKEHVMSSIIITHVSDSPFGWTATGCVQFVTRNADLTIED 252
QY 163 LKYYAD 168
Db 253 VEDLAE 258
RESULT 8
Q4ZV84_PSESY PRELIMINARY; PRT; 914 AA.
AC Q4ZV84_PSESY PRELIMINARY; PRT; 914 AA.
DT 13-SEP-2005 (TremBLrel. 31, Created)
DT 13-SEP-2005 (TremBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TremBLrel. 31, Last annotation update)
DE SNP2-related:Helicase, C-terminal:SWIM Zn-finger.
GN ORFNames=PeY_1894;
OS Pseudomonas syringae pv. syringae B728a.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=205918;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=B728a;
RG DOE Joint Genome Institute;
RA Chain P., Larimer F., DiBartolo G., Copeland A., Lykidis A., Trong S., Nolan M., Goltsman E., Thiel J., Malfatti S., Lapidus A., Detter J.C., Land M., Richardson P.M., Kyrpides N.C., Ivanova N.;
RA "Comparison of two complete genome sequences of Pseudomonas syringae pv. syringae B728a and pv. tomato DC3000.";
RL Proc. Natl. Acad. Sci. U.S.A. 0:0-0(2005).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=B728a;
RA Loper J.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=B728a;
RA Feil H., Feil W.S., Lindow S.E.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; CP000075; AAY36938.1; -; Genomic DNA.
DR GO; GO:0004386; F:helicase activity; IEA.
KW Helicase.
SQ SEQUENCE 914 AA; 104114 MW; 3C9DD8894DF84B5E CRC64;
Query Match 9.4%; Score 89.5; DB 2; Length 914;
Best Local Similarity 26.2%; Pred. No. 33;
Matches 34; Conservative 19; Mismatches 50; Indels 27; Gaps 4;
QY 62 RLLOVRRPVALEALTLK-----VLEAAAGPALSD--VLQOPLHLHL 107
Db 421 RLNIKADPVSPLDGLNATLRYQLEGLSNMQSLRELVGGVLADDMGLGKTLQTLAHL 480

QY 108 SOLOACIQPQTAGPRGRHLHWLHR-----LQAPKESAGCL-EASVTEN 154
Db 481 MEKQAGRLDRPALAVMPTSLIPNWLDESEHTPDLKVLALYGNRHRQDAGNLQDYDLILT 540
QY 155 LFRLLTRDLK 164
Db 541 TVALLPRDLE 550
RESULT 9
Q8G5G0_BIFLO PRELIMINARY; PRT; 296 AA.
AC Q8G5G0;
DT 01-MAR-2003 (TremBLrel. 23, Created)
DT 01-MAR-2003 (TremBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TremBLrel. 23, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=BL1052;
OS Bifidobacterium longum.
OC Bacteria; Actinobacteria; Actinobacteriales; Bifidobacteriales;
OC Bifidobacteriaceae; Bifidobacterium.
OX NCBI_TaxID=216816;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=NCC 2705;
RX MEDLINE=22294977; PubMed=12381787; DOI=10.1073/pnas.212527599;
RA Schell M.A., Kamirantzou M., Snel B., Vilanova D., Berger B., Pessi G., Zwielen M.-C., Desiere F., Bork P., Delley M., Pridmore R.D., Arigoni F.;
RA "The genome sequence of Bifidobacterium longum reflects its adaptation to the human gastrointestinal tract.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427(2002).
DR EMBL; AE014295; AAM24858.1; -; Genomic DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 296 AA; 33881 MW; 54E29BC63276994E CRC64;
Query Match 9.3%; Score 89; DB 2; Length 296;
Best Local Similarity 28.9%; Pred. No. 9.8;
Matches 39; Conservative 19; Mismatches 55; Indels 22; Gaps 8;
QY 46 KMW-SCSSPPFGNWDRL-LQVRRPVALEALTLKYLEAAG-----PALEDVLD 97
Db 14 RTWRQCRTPAEPRDSVKRLILAAAHKFAQKVDVLTIRHLEGLEHTLLCVDDAID 73
QY 98 QPLHTLHLSOLOACIQPQTAGPR--GRHLHWLRLQAPKESAGCLEASVTNL 155
Db 74 GPAQTLNRILRLKTHPVGYR-TGAPLPRATGACRHLHLRDG-----IEHLEPEH 124
QY 156 FRLLTRDLKVVADGN 170
Db 125 AR--NRD-RQVDDGD 136
RESULT 10
Q8DJL0_SYNEL PRELIMINARY; PRT; 458 AA.
AC Q8DJL0_SYNEL PRELIMINARY; PRT; 458 AA.
DT 01-MAR-2003 (TremBLrel. 23, Created)
DT 01-MAR-2003 (TremBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Isochorismate synthase.
GN OrderedLocusNames=tll1213;
OS Synecococcus elongatus (Thermosynechococcus elongatus).
OC Bacteria; Cyanobacteria; Chroococcales; Synecococcus.
OX NCBI_TaxID=32046;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BP-1;
RX MEDLINE=2225144; PubMed=12240834;
RA Nakamura Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamoto S., Watanabe A., Iriiguchi M., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Nakazaki N.,

RA Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D.,
 RA Olsen G.J., Sogin M.L.,
 RT "Draft sequence of the Giardia lamblia genome."
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 preliminary data.
 DR EMBL; AACB01000042; EAA040466.1; -; Genomic DNA.
 SQ SEQUENCE 479 AA; 53677 MW; 70F50040A717818C CRC64;

Query Match 9.1%; Score 87; DB 2; Length 479;
 Best Local Similarity 25.6%; Pred. No. 26;
 Matches 45; Conservative 23; Mismatches 56; Indels 52; Gaps 7;

QY 11 TTGKGCHIGRFXSLSPQELASPKKARDALLESLSK-----LKNWSSSPVFGNWDRLQLQVRE 70
 DB TSASIKIKKREKDLK-----AAYKQKEAYEQ-MKQKWSA----- 73

QY 71 VALEAEALTLTKVLEAAAGPAL--EDVLDQPLHTLHHI-----LSQLQACIQPQ 117
 DB ---EALNGQLAVLEAKKESLIMTKIMEQVHLDLDDIKTKNSLDLAQLAFLQSNLKG 130

QY 118 PTAGPRPRGRLLHWHRLHQEAPKESAGCLEASVTFNFLRLTRDLKLVADGNLSL 173
 DB 131 ATEKANMRSVLRDAKHRLHY-LKECEGLLDAQ-----KOLEHSIIEALSIL 175

RESULT 14
 Q5B9M4 EMENI PRELIMINARY; PRT; 967 AA.
 AC Q5B9M4;
 DT 10-MAY-2005 (TremBLrel. 30, Created)
 DT 10-MAY-2005 (TremBLrel. 30, Last sequence update)
 DE Hypothetical protein.
 GN ORFNames=AN2756.2;
 OS Aspergillus nidulans FGSC A4.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eutotiales; Trichocomaceae; Emericella.
 OX NCBI_TaxID=227321;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=FGSC A4;
 RA Birren B., Nusbaum C., Abouelleil A., Allen N., Anderson S.,
 RA Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavsky L.,
 RA Bookhgalter B., Butler J., Calvo S.E., Camarata J., Chang J.,
 RA Choepel Y., Collymore A., Cook K., Cooke P., Corum B., Dearellano K.,
 RA Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,
 RA Erickson J., Faro S., Ferreira P., FitzGerald M., Gage D., Galagan J.,
 RA Gardyna S., Gnerre S., Graham L., Grand-pierre N., Hafez N.,
 RA Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,
 RA Jaffe D., Johnson R., Jones C., Kamal M., Kamat A., Karatas A.,
 RA Kells C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,
 RA Ma L.-J., Mabbitt R., McLean C., Macdonald P., Major J., Manning J.,
 RA Matthews C., Mauceli E., McCarthy M., Meldrim J., Meneus L.,
 RA Mihova T., Mienga V., Murphy T., Naylor J., Nguyen C., Nicol R.,
 RA Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neil D.,
 RA Oliver J., Peterson K., Phunkhang P., Pierre N., Purcell S.,
 RA Rachupka A., Ramasamy U., Raymond C., Retta R., Rise C., Rogov P.,
 RA Roman J., Schauer S., Schupbach R., Seaman S., Severy P., Smirnov S.,
 RA Smith C., Spencer B., Stange-Thomann N., Stojanovic N., Stubbs M.,
 RA Talamas J., Tesfaye S., Theodore J., Topham K., Travers M.,
 RA Vasiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,
 RA Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,
 RA Lander E.;
 RT "Genome Sequence of Aspergillus nidulans."
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 preliminary data.
 DR EMBL; AACB01000049; EAG63190.1; -; Genomic DNA.
 KW Hypothetical protein.
 SQ SEQUENCE 967 AA; 109021 MW; 9BC297B7E10A1159 CRC64;

Query Match 9.1%; Score 86.5; DB 2; Length 967;
 Best Local Similarity 25.6%; Pred. No. 67;
 Matches 50; Conservative 28; Mismatches 62; Indels 55; Gaps 11;

QY 14 KGCHIGRFXSLSPQELASPKKARDALLESLSK-----LKNWSSSPVFGNWDRLQLQVRE 68
 DB 461 KGTEISSLLSKYNREMA-----LEALRNKTRALEEYTKNEMRNGDHELAL---RE 510

QY 69 RPVALEA-----ELALTLKVLAAAGPALEDVLDPL-HTLHHLSQLQACIQPQPTAG 121
 DB 511 KETELANQAAMDEALLEELKLSQGDAD-KALDPTQIDHVLHGTSTVKINDIIDSVLQGT 569

QY 122 PRPRGRLLHWHRLHQE-----AP-----KESAGCLEASVTFNFLRLTRDLK 165
 DB 570 VQ---RVDALYELDSTWQAGNQNASPPYVLSQIEKASASATEFTAFN-----NY 617

QY 166 VADGNLSLRTSTHPE 180
 DB 618 ISDG---PNSPHAE 628

RESULT 15
 Q58D46 BOVIN PRELIMINARY; PRT; 333 AA.
 AC Q58D46;
 DT 10-MAY-2005 (TremBLrel. 30, Created)
 DT 10-MAY-2005 (TremBLrel. 30, Last sequence update)
 DE Rab geranylgeranyltransferase, alpha subunit.
 GN Name=RABGGTA;
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
 OC Pecora; Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Pooled;
 RX MEDLINE=21180013; PubMed=11282978; DOI=10.1101/gr.170101;
 RA Smith T.P.L., Grosse W.M., Freking B.A., Roberts A.J., Stone R.T.,
 RA Casas E., Wray J.E., White J., Cho J., Fahrenkrug S.C., Bennett G.L.,
 RA Heaton M.P., Laegreid W.W., Rohrer G.A., Chitko-McKown C.G.,
 RA Perteau G., Holt I., Karamycheva S., Liang F., Quackenbush J.,
 RA Keefe J.W.;
 RT "Sequence evaluation of four pooled-tissue normalized bovine cDNA
 libraries and construction of a gene index for cattle."
 RL Genome Res. 11:626-630(2001).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Pooled;
 RA Harhay G.P., Sonstegard T.S., Van Tassel C.P., Clawson M.L.,
 RA Heaton M.P., Keefe J.W., Snelling W.M., Weidmann R.T., Smith T.P.L.;
 RT "Sequencing and analysis of Bos taurus full-length insert cDNA
 clones."
 RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BT021751; AAX46598.1; -; mRNA.
 DR GO; GO:0008318; F:protein prenyltransferase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0018346; P:protein amino acid prenylation; IEA.
 KW Prenyltransferase; Repeat; Transferase.
 SQ SEQUENCE 333 AA; 38129 MW; 4B92E0657332777A CRC64;

Query Match 9.0%; Score 86; DB 2; Length 333;
 Best Local Similarity 27.2%; Pred. No. 21;
 Matches 53; Conservative 18; Mismatches 54; Indels 70; Gaps 10;

QY 25 SPQELASPKKAR-DALLESLSKLNWSSSPVFGNWDRL---LLQVRPVALEAL-AL 79
 DB 81 SPEELATLVKAEGLFLESCLV-----NPKSYGTWHHRCWLLSLPFPNWARELELCAR 134

QY 80 TLKV-----LEAAAGPALEDVLDQPLHTLH-----HLSQLQACIQPQ 117

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OM protein - protein search, using sw model

Run on: December 29, 2005, 13:47:02 ; Search time 38 Seconds
(without alignments)
460.828 Million cell updates/sec

Title: US-10-691-923-34
Perfect score: 955
Sequence: 1 MGPVTSKPTTGGKCHGR.....LKYVADGNLSLRTSTHPST 182

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	83	8.7	567	JC5538	Rab geranylgeranyl
2	82	8.6	899	S12319	pre-mRNA splicing
3	81.5	8.5	530	S52215	hypothetical prote
4	81.5	8.5	553	C75318	hypothetical prote
5	81.5	8.5	1086	B46335	HIV-1 retropepsin
6	80.5	8.4	468	T35928	probable aldehyde
7	80.5	8.4	1101	B45390	HIV-1 retropepsin
8	80.5	8.4	1101	GHLJVS	HIV-1 retropepsin
9	79.5	8.3	271	S27282	Bl496_F2.81 protei
10	79.5	8.3	1087	JQ1162	Poi protein - Maed
11	79	8.3	495	S27083	probable accD3 pro
12	79	8.3	557	T24538	hypothetical prote
13	78.5	8.2	253	A00251	high-affinity zinc
14	78.5	8.2	942	JC2129	protein kinase PN
15	77.5	8.1	217	H64186	hypothetical prote
16	77.5	8.1	371	E72665	hypothetical prote
17	77.5	8.1	946	JC2130	protein kinase (EC
18	77.5	8.1	1035	A64686	cation efflux syst
19	77	8.1	775	T41961	hypothetical prote
20	77	8.1	3788	T13960	beige protein homo
21	76.5	8.0	1035	D71831	cation efflux syst
22	76	8.0	191	S57642	interferon precurs
23	76	8.0	528	C83033	benzoylformate dec
24	75.5	7.9	403	S76603	hypothetical prote
25	75.5	7.9	559	A23325	DNA repair protein
26	75.5	7.9	581	A41923	hypothetical prote
27	75.5	7.9	649	JQ0103	hypothetical 70K p
28	75.5	7.9	654	I56134	tumor necrosis fac
29	75	7.9	640	S37869	probable serine/th

30	75	7.9	679	2	AE0694	probable membrane
31	74.5	7.8	221	2	T39198	Ram/Rab27 - human
32	74.5	7.8	268	2	S76063	hypothetical prote
33	74.5	7.8	373	2	A44478	probable cell grow
34	74.5	7.8	786	2	F70735	hypothetical prote
35	74	7.7	339	2	AI3609	daunorubicin resis
36	74	7.7	1007	2	T13693	hypothetical prote
37	73.5	7.7	189	2	JC7891	testis expressed 2
38	73.5	7.7	392	2	T43490	hypothetical prote
39	73.5	7.7	739	2	S32948	hyf protein - Rho
40	73.5	7.7	845	2	T00071	hypothetical prote
41	73.5	7.7	1012	2	T13712	dof protein - frui
42	73.5	7.7	1144	2	T13749	dof protein - frui
43	73.5	7.7	3856	2	T51174	ataxia-telangiecta
44	73	7.6	218	2	A47285	milk fat globule p
45	73	7.6	567	2	A45977	Rab geranylgeranyl

ALIGNMENTS

RESULT 1

JC5538
Rab geranylgeranyl transferase (EC 2.5.1.-) alpha chain - human
C:Species: Homo sapiens (man)
C:Date: 02-Sep-1997 #sequence_revision 05-Sep-1997 #text_change 09-Jul-2004
C:Accession: JC5538
R:Song, H.J.; Rossi, A.; Ceci, R.; Kim, I.G.; Anzano, M.A.; Jang, S.I.; De Laurenzi, V.
Biochem. Biophys. Res. Commun. 235, 10-14, 1997
A:Title: The genes encoding geranylgeranyl transferase alpha-subunit and transglutamina
A:Reference number: JC5538; MUID:97339427; PMID:9196026
A:Accession: JC5538
A:Molecule type: DNA
A:Residues: 1-567 <SON>
A:Cross-references: UNIPROT:Q92696; UNIPARC:UPI000013188E
C:Comment: This protein is involved in cutaneous disease. The gene of this enzyme is po
C:Genetics:
A:Gene: Rabggt
A:Introns: 1/3; 38/3; 81/1; 143/1; 211/1; 238/2; 278/3; 300/3; 336/2; 354/2; 383/2; 413
C:Keywords: transférase

Query Match	8.7%	Score 83;	DB 2;	Length 567;
Best Local Similarity	25.6%	Pred. No. 7.9;		
Matches	50;	Conservative 16;	Mismatches 59;	Indels 70; Gaps 9;
QY	25	SQELASFKKAR-DALRESLKLKNSCSSPFGNWDLRLLQVRPVA-LEAELALTLK	82	
DB	81	SPEELAAVKAELGFLSCLRV-----NPKSYGTWHRCWLLGLRLPEPNWTRLELCAR	134	
QY	83	VLE-----AAAGPALEDVLDQPLHTLH-----HLSQLQACIQPQ	117	
DB	135	FLEVDERNFHCWYRRFVATQAVPAEELAFDTSLTRNFSNYSWYRSCLLPQLHPQ	194	
QY	118	PTAGPRPRGRU-----HHWLHRLQAPKKESAGCL--	147	
DB	195	PDSG--PQGRLPEDVLLKLELVQNAFTDNDQSAWPFYRWL--LGRADPDALRCLHV	250	
QY	148	---EASTFNFRLLL	159	
DB	251	SRDEACLTVSFSRPL	265	

RESULT 2

S12319
pre-mRNA splicing factor PRP6 - yeast (Saccharomyces cerevisiae)
N:Alternate names: protein YBR0508; protein YBR055C
C:Species: Saccharomyces cerevisiae
C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 09-Jul-2004
C:Accession: S12319; S49513; S49510; S55854
R:Legrain, P.; Choulika, A.
EMBO J. 9, 2775-2781, 1990
A:Title: The molecular characterization of PRP6 and PRP9 yeast genes reveals a new cyst
A:Reference number: S12319; MUID:90360988; PMID:2118103

A:Accession: B45390
A:Molecule type: DNA
A:Residues: 1-1101 <AND>
C:Cross-references: UNIPARC:UPI0000131F26; GB:S55323; NID:g265825; PIDN:AAB25460.1; PIR:
C:Comment: Specific enzymatic cleavages may yield mature proteins including proteinase,
C:Genetics:
A:Gene: pol
C:Superfamily: pol polyprotein
C:Keywords: AIDS; aspartic proteinase; endonuclease; hydrolase; immunodeficiency; nucle
F:35-135/Product: retropepsin #status predicted <RTP>
F:144-856/Product: RNA-directed DNA polymerase #status predicted <REV>
F:857-1101/Product: endonuclease #status predicted <ENC>
F:59/Active site: Asp (shared with dimeric partner) #status predicted

Query Match 8.4%; Score 80.5; DB 1; Length 1101;
Best Local Similarity 31.6%; Pred. No. 30;
Matches 25; Conservative 16; Mismatches 23; Indels 15; Gaps 5;

QY 14 KGCHIGFKSLSPOLASFKKARDALRESLKL-----KNWSCSSPVF-----PGNW----D 60
DB 155 KGPHAQW-PUTQBKJGLKEIVDRLEKGKVGRRAPPHWTNTPIFCIKKSGKWRMLID 213
QY 61 LRLQLVRRPVALEAEAL 79
DB 214 FRELNKQTEDIA-EAQJGL 231

RESULT 8
GNLJVS
HIV-1 retropepsin (EC 3.4.23.16) - Maedi/Visna virus (strain 1514)
N:Contains: endonuclease (EC 3.1.-.-); retropepsin (EC 3.4.23.16); RNA-directed DNA pol
C:Species: Maedi/Visna virus
A>Note: host Homo sapiens (man)
C:Date: 28-Feb-1996 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C:Accession: A03969
R:Sonigo, P.; Alison, M.; Staskus, K.; Klatzmann, D.; Cole, S.; Danos, O.; Retzel, E.;
Cell 42, 369-382, 1985
A>Title: Nucleotide sequence of the visna lentivirus: relationship to the AIDS virus.
A:Reference number: A90869; MUID:85254938; PMID:2410140
A:Accession: A03969
A:Molecule type: DNA
A:Residues: 1-1101 <SON>
C:Cross-references: UNIPROT:P03370; UNIPARC:UPI000011D50A; GB:M10608
C:Comment: Specific enzymatic cleavages may yield mature proteins including proteinase,
C:Genetics:
A:Gene: pol
C:Superfamily: pol polyprotein
C:Keywords: AIDS; aspartic proteinase; endonuclease; hydrolase; immunodeficiency; nucle
F:35-135/Product: retropepsin #status predicted <RTP>
F:144-856/Product: RNA-directed DNA polymerase #status predicted <REV>
F:857-1101/Product: endonuclease #status predicted <ENC>
F:59/Active site: Asp (shared with dimeric partner) #status predicted

Query Match 8.4%; Score 80.5; DB 1; Length 1101;
Best Local Similarity 31.6%; Pred. No. 30;
Matches 25; Conservative 16; Mismatches 23; Indels 15; Gaps 5;

QY 14 KGCHIGFKSLSPOLASFKKARDALRESLKL-----KNWSCSSPVF-----PGNW----D 60
DB 155 KGPHAQW-PUTQBKJGLKEIVDRLEKGKVGRRAPPHWTNTPIFCIKKSGKWRMLID 213
QY 61 LRLQLVRRPVALEAEAL 79
DB 214 FRELNKQTEDIA-EAQJGL 231

RESULT 9
S72782
B1496_F2_81 protein - Mycobacterium leprae
C:Species: Mycobacterium leprae
C:Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C:Accession: S72782
R:Smith, D.R.; Robison, K.

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 29, 2005, 13:29:22 ; Search time 187 Seconds
(without alignments)
427.631 Million cell updates/sec

Title: US-10-691-923-34

Perfect score: 955

Sequence: 1 MGVPVTSKPTTGKCHIGR.....LKYVADGNLSLRTSTHPEST 182

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq 21:*

- 1: Geneseq1980s:*
- 2: Geneseq1990s:*
- 3: Geneseq2000s:*
- 4: Geneseq2001s:*
- 5: Geneseq2002s:*
- 6: Geneseq2003as:*
- 7: Geneseq2003bs:*
- 8: Geneseq2004s:*
- 9: Geneseq2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	955	100.0	182	8	Ado59974 Met IL-28
2	955	100.0	182	9	Ady03602 Human IL-
3	951	98.6	182	9	Ady03614 Human IL-
4	950	99.5	181	8	Ado59972 IL-28A mu
5	950	99.5	181	9	Ady03600 Human IL-
6	950	99.5	182	8	Ado59978 Met IL-29
7	950	99.5	182	9	Ady03588 Human IL-
8	948	98.3	183	9	Ady03724 Human IL-
9	947	99.2	183	9	Ady03728 Human IL-
10	946	99.1	181	9	Ady03613 Human IL-
11	946	99.1	182	9	Ady03658 Human IL-
12	946	99.1	185	9	Ady03734 Human IL-
13	945	99.0	182	9	Ady03662 Human IL-
14	945	99.0	200	5	Aae18311 Human Zcy
15	945	99.0	200	5	Aae18310 Human Zcy
16	945	99.0	200	8	Ado59960 IL-29. 7/
17	945	99.0	200	8	Ady03577 Human IL-
18	944	98.8	182	9	Ady03678 Human IL-
19	941	98.5	181	9	Ady03656 Human IL-
20	941	98.5	182	9	Ady03730 Human IL-
21	941	98.5	182	9	Ady03726 Human IL-
22	940	98.4	180	9	Ady03712 Human IL-
23	940	98.4	181	9	Ady03660 Human IL-
24	940	98.4	182	9	Ady03670 Human IL-

25	940	98.4	200	5	AAU83208	Novel sec
26	940	98.4	200	5	AAE18309	Human Zcy
27	940	98.4	200	6	AAE32761	Human zcy
28	940	98.4	200	7	AdfB3645	Human cyt
29	940	98.4	200	8	Ado59944	IL-29. 7/
30	940	98.4	203	5	AAE18313	Human Zcy
31	940	98.4	219	5	AAE18312	Human Zcy
32	939	98.3	181	9	Ady03676	Human IL-
33	939	98.3	182	9	Ady03650	Human IL-
34	939	98.3	182	9	Ady03686	Human IL-
35	939	98.3	200	7	AdC17329	Human IFN
36	938	98.2	200	6	AAO16278	Human IMX
37	935	97.9	181	9	Ady03668	Human IL-
38	934	97.8	181	9	Ady03648	Human IL-
39	934	97.8	181	9	Ady03684	Human IL-
40	934	97.8	182	9	Ady03654	Human IL-
41	933	97.7	179	9	Ady03714	Human IL-
42	933	97.7	182	9	Ady03666	Human IL-
43	932	97.6	182	9	Ady03682	Human IL-
44	929	97.3	178	9	Ady03716	Human IL-
45	929	97.3	181	9	Ady03652	Human IL-

ALIGNMENTS

RESULT 1

ADo59974

ID AD059974 standard; protein; 182 AA.

XX AC AD059974;

XX DT 29-JUL-2004 (first entry)

XX DE Met IL-28A mutant C172S.

XX KW interleukin; IL-28A; IL-28B; viral; infection; liver; inflammation;

XX KW viral load; anti-viral antibody; serological level;

XX KW alanine aminotransferase; histological improvement; hepatitis B;

XX KW hepatitis C; cytopaenia; leukocyte deficiency; neutropenia;

XX KW thrombocytopenia; anaemia; IL-29.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT Misc-difference 172

XX FT Misc-difference 172

XX FT Misc-difference 172

XX FT Misc-difference 172

XX FT Misc-difference 172

XX FT Misc-difference 172

XX FT Misc-difference 172

XX FT Misc-difference 172

XX FT Misc-difference 172

XX FT Misc-difference 172

XX FT Misc-difference 172

XX FT Misc-difference 172

XX FT Misc-difference 172

XX FT Misc-difference 172

XX FT Misc-difference 172

XX FT Misc-difference 172

XX FT Misc-difference 172

XX FT Misc-difference 172

XX FT Misc-difference 172

XX FT Misc-difference 172

XX FT Misc-difference 172

XX FT Misc-difference 172

XX FT Misc-difference 172

XX FT Misc-difference 172

XX FT Misc-difference 172

XX FT Misc-difference 172

XX FT Misc-difference 172

XX FT Misc-difference 172

XX FT Misc-difference 172

XX FT Misc-difference 172

XX FT Misc-difference 172

XX FT Misc-difference 172

XX FT Misc-difference 172

XX FT Misc-difference 172

XX FT Misc-difference 172

XX FT Misc-difference 172

XX FT Misc-difference 172

CC This sequence represents a mutant interleukin IL-28A, Met-C172S. This
 CC interleukin protein may be used in the method of the invention for
 CC treating a viral infection. The method comprises administering to a
 CC mammal with a viral infection causing liver inflammation, an interleukin-
 CC based polypeptide, where the viral infection level or liver inflammation
 CC is reduced. The reduction in the viral infection level is measured as a
 CC decrease in viral load, an increase in anti-viral antibodies, a decrease
 CC in serological levels of alanine aminotransferase or histological
 CC improvement. The viral infection is hepatitis B or C virus infection. The
 CC mammal has cytopaenia, comprising leukocyte deficiency, neutropenia,
 CC thrombocytopenia or anaemia. The interleukin polypeptide is interleukin
 CC 28 or 29, or a variant of these. The method of the invention is useful in
 CC treating hepatitis B or C virus infection.

XX Sequence 182 AA;

Query Match 100.0%; Score 955; DB 8; Length 182;
 Best Local Similarity 100.0%; Pred. No. 2.8e-91;
 Matches 182; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGPVPTSKPTTGGCHIGRFKSLSPQELASFKKARDALEESLKLNWSSCSPPVPGNWD 60
 Db 1 MGPVPTSKPTTGGCHIGRFKSLSPQELASFKKARDALEESLKLNWSSCSPPVPGNWD 60

Qy 61 LRLQVRPVALEAEALTLKYLEAAAGPALEDVLDQPLHTLHHLSOLOQACIQOPTA 120
 Db 61 LRLQVRPVALEAEALTLKYLEAAAGPALEDVLDQPLHTLHHLSOLOQACIQOPTA 120

Qy 121 GPRPRGLHHLRLQEAAPKESAGCLEASVTFFNLLTRDLKYVADGNLSLRTSTHPE 180
 Db 121 GPRPRGLHHLRLQEAAPKESAGCLEASVTFFNLLTRDLKYVADGNLSLRTSTHPE 180

Qy 181 ST 182
 Db 181 ST 182

RESULT 2

ADY03602
 ID ADY03602 standard; protein; 182 AA.

XX AC ADY03602;

XX 05-MAY-2005 (first entry)

XX Human IL-29 mutant protein sequence SeqID29.

XX antiviral; pharmaceutical; hepatitis b virus infection;
 KW hepatitis c virus infection; mutant; mutein; IL-29.

XX Homo sapiens.

OS Synthetic.

XX US2005037012-A1.

XX 17-FEB-2005.

XX 09-AUG-2004; 2004US-00914772.

XX 07-AUG-2003; 2003US-0493194P.

PR 10-MAR-2004; 2004US-0551841P.

PR 02-APR-2004; 2004US-0559142P.

PA (BRAD/) BRADY L J.

PA (KLUC/) KLUCHER K M.

PA (CHAN/) CHAN C.

PA (DONG/) DONG D L.

PA (LIUH/) LIU H Y.

PA (SHEP/) SHEPPARD P O.

PA (BUKO/) BUKOWSKI T R.

XX Brady LJ, Klucher KM, Chan C, Dong DL, Liu HY, Sheppard PO;

PI Bukowski TR;

XX WPI; 2005-180368/19.
 DR N-PGDB; ADY03601.

PT Novel isolated Interleukin-28A, IL-28B or IL-29 polypeptide having anti-
 PT viral activity, useful for treating hepatitis B or hepatitis C
 PT infections.

XX Claim 1; SEQ ID NO 29; 149pp; English.

XX This invention relates to a novel isolated IL-28A, IL-28B or IL-29
 CC polypeptide having antiviral activity. One or more of the cysteine
 CC residues were mutated to produce the proteins of the invention. The
 CC invention may be useful for the development of a pharmaceutical
 CC composition for the treatment of hepatitis B or C. The present sequence
 CC is that of a novel IL variant protein of the invention.

XX Sequence 182 AA;

Query Match 100.0%; Score 955; DB 9; Length 182;
 Best Local Similarity 100.0%; Pred. No. 2.8e-91;
 Matches 182; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGPVPTSKPTTGGCHIGRFKSLSPQELASFKKARDALEESLKLNWSSCSPPVPGNWD 60
 Db 1 MGPVPTSKPTTGGCHIGRFKSLSPQELASFKKARDALEESLKLNWSSCSPPVPGNWD 60

Qy 61 LRLQVRPVALEAEALTLKYLEAAAGPALEDVLDQPLHTLHHLSOLOQACIQOPTA 120
 Db 61 LRLQVRPVALEAEALTLKYLEAAAGPALEDVLDQPLHTLHHLSOLOQACIQOPTA 120

Qy 121 GPRPRGLHHLRLQEAAPKESAGCLEASVTFFNLLTRDLKYVADGNLSLRTSTHPE 180
 Db 121 GPRPRGLHHLRLQEAAPKESAGCLEASVTFFNLLTRDLKYVADGNLSLRTSTHPE 180

Qy 181 ST 182
 Db 181 ST 182

RESULT 3

ADY03614

ID ADY03614 standard; protein; 182 AA.

XX AC ADY03614;

XX 05-MAY-2005 (first entry)

XX Human IL-28A mutant protein sequence SeqID41.

XX antiviral; pharmaceutical; hepatitis b virus infection;
 KW hepatitis c virus infection; mutant; mutein; IL-28A.

XX Homo sapiens.

OS Synthetic.

XX US2005037012-A1.

XX 17-FEB-2005.

XX 09-AUG-2004; 2004US-00914772.

XX 07-AUG-2003; 2003US-0493194P.

PR 10-MAR-2004; 2004US-0551841P.

PR 02-APR-2004; 2004US-0559142P.

PA (BRAD/) BRADY L J.

PA (KLUC/) KLUCHER K M.

PA (CHAN/) CHAN C.

PA (DONG/) DONG D L.

PA (LIUH/) LIU H Y.

PA (SHEP/) SHEPPARD P O.

PA (BUKO/) BUKOWSKI T R.


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XX PI Brady LJ, Klucher KM, Chan C, Dong DL, Liu HY, Sheppard PO;
XX PI Bukowski TR;
XX DR WPI; 2005-180368/19.
XX DR N-PSDB; ADY03608.
XX PT Novel isolated Interleukin-28A, IL-28B or IL-29 polypeptide having anti-
XX PT viral activity, useful for treating hepatitis B or hepatitis C
XX PT infections.
XX PS Claim 1; SEQ ID NO 41; 149pp; English.
XX CC This invention relates to a novel isolated IL-28A, IL-28B or IL-29
XX CC polypeptide having antiviral activity. One or more of the cysteine
XX CC residues were mutated to produce the proteins of the invention. The
XX CC invention may be useful for the development of a pharmaceutical
XX CC composition for the treatment of hepatitis B or C. The present sequence
XX CC is that of a novel IL variant protein of the invention.
XX SQ Sequence 182 AA;

Query Match 99.6%; Score 951; DB 9; Length 182;
Best Local Similarity 99.5%; Pred. No. 7.3e-91;
Matches 181; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGVPVTSKPTTGGCHIGRFKSLSPQELASFKKARDALAEESLKLNWSCSSPVFGNWD 60
DB 1 MGVPVTSKPTTGGCHIGRFKSLSPQELASFKKARDALAEESLKLNWSCSSPVFGNWD 60
QY 61 LRLQVRERPVVALEAEALTLTKVLEAAAGPALEDVLDQPLHTLHILSLQACIQPQPTA 120
DB 61 LRLQVRERPVVALEAEALTLTKVLEAAAGPALEDVLDQPLHTLHILSLQACIQPQPTA 120
QY 121 GPRGRHLHHLRLQEAAPKESAGCLEASVTNLFRLTLTRDLKYVADGNLSLRTSTHPE 180
DB 121 GPRGRHLHHLRLQEAAPKESAGCLEASVTNLFRLTLTRDLKYVADGNLSLRTSTHPE 180
QY 181 ST 182
DB 181 ST 182

RESULT 4
AD059972
ID AD059972 standard; protein; 181 AA.
XX AC AD059972;
XX DT 29-JUL-2004 (first entry)
XX DE IL-28A mutant C171S.
XX KW interleukin; IL-28A; IL-28B; viral; infection; liver; inflammation;
XX KW viral load; anti-viral antibody; serological level;
XX KW alanine aminotransferase; histological improvement; hepatitis B;
XX KW hepatitis C; cytopenia; leukocyte deficiency; neutropenia;
XX KW thrombocytopenia; anaemia; IL-29.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT Misc-difference 171 /label= C171S
XX PN WO2004037995-A2.
XX PD 06-MAY-2004.
XX PF 23-OCT-2003; 2003WO-US033628.
XX PR 23-OCT-2002; 2002US-0420713P.
XX PR 23-OCT-2002; 2002US-0420714P.

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PR 18-APR-2003; 2003US-0463939P.
PR 18-APR-2003; 2003US-0463982P.
XX PA (ZYMO ) ZYMOGENETICS INC.
XX PI Klucher KM, Sivakumar PV, Kindsvogel WR, Henderson KE;
XX DR WPI; 2004-365507/34.
XX DR N-PSDB; AD059971.
XX PT Treating hepatitis B or hepatitis C virus infection comprises
XX PT administering to a mammal with a viral infection causing liver
XX PT inflammation, a polypeptide that is conjugated to a polyalkyl oxide
XX PT group.
XX PS Claim 12; SEQ ID NO 32; 102pp; English.
XX CC This sequence represents a mutant interleukin IL-28A, Met-C171S. This
XX CC interleukin protein may be used in the method of the invention for
XX CC treating a viral infection. The method comprises administering to a
XX CC mammal with a viral infection causing liver inflammation, an interleukin-
XX CC based polypeptide, where the viral infection level or liver inflammation
XX CC is reduced. The reduction in the viral infection level is measured as a
XX CC decrease in viral load, an increase in anti-viral antibodies, a decrease
XX CC in serological levels of alanine aminotransferase or histological
XX CC improvement. The viral infection is hepatitis B or C virus infection. The
XX CC mammal has cytopenia, comprising leukocyte deficiency, neutropenia,
XX CC thrombocytopenia or anaemia. The interleukin polypeptide is interleukin
XX CC 28 or 29, or a variant of these. The method of the invention is useful in
XX CC treating hepatitis B or C virus infection.
XX SQ Sequence 181 AA;

Query Match 99.5%; Score 950; DB 8; Length 181;
Best Local Similarity 100.0%; Pred. No. 9.2e-91;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GPVPTSKEPTTGGCHIGRFKSLSPQELASFKKARDALAEESLKLNWSCSSPVFGNWD 61
DB 1 GPVPTSKEPTTGGCHIGRFKSLSPQELASFKKARDALAEESLKLNWSCSSPVFGNWD 60
QY 62 RLLQVRERPVVALEAEALTLTKVLEAAAGPALEDVLDQPLHTLHILSLQACIQPQPTAG 121
DB 61 RLLQVRERPVVALEAEALTLTKVLEAAAGPALEDVLDQPLHTLHILSLQACIQPQPTAG 120
QY 122 PRPRGRHLHHLRLQEAAPKESAGCLEASVTNLFRLTLTRDLKYVADGNLSLRTSTHPE 181
DB 121 PRPRGRHLHHLRLQEAAPKESAGCLEASVTNLFRLTLTRDLKYVADGNLSLRTSTHPE 180
QY 182 T 182
DB 181 T 181

RESULT 5
ADY03600
ID ADY03600 standard; protein; 181 AA.
XX AC ADY03600;
XX DT 05-MAY-2005 (first entry)
XX DE Human IL-29 mutant protein sequence SeqID27.
XX KW antiviral; pharmaceutical; hepatitis b virus infection;
XX KW hepatitis c virus infection; mutant; mutein; IL-29.
XX OS Homo sapiens.
XX OS Synthetic.
XX PN US2005037012-A1.
XX PD 17-FEB-2005.

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XX 09-AUG-2004; 2004US-00914772.
XX PF
XX 07-AUG-2003; 2003US-0493194P.
XX PR
XX 10-MAR-2004; 2004US-0551841P.
XX PR
XX 02-APR-2004; 2004US-0559142P.
XX PR
XX (BRAD//) BRADY L J.
XX PA
XX (KLUC//) KLUCHER K M.
XX PA
XX (CHAN//) CHAN C.
XX PA
XX (DONG//) DONG D L.
XX PA
XX (LIUH//) LIU H Y.
XX PA
XX (SHEP//) SHEPPARD P O.
XX PA
XX (BUKO//) BUKOWSKI T R.
XX PA
XX Brady LJ, Klucher KM, Chan C, Dong DL, Liu HY, Sheppard PO;
XX PI Bukowski TR;
XX PI
XX WPI; 2005-180368/19.
XX DR N-PSDB; ADY03599.
XX DR
XX Novel isolated interleukin-28A, IL-28B or IL-29 polypeptide having anti-
XX PT viral activity, useful for treating hepatitis B or hepatitis C
XX PT infections.
XX PT
XX Claim 1; SEQ ID NO 27; 149pp; English.
XX PS
XX This invention relates to a novel isolated IL-28A, IL-28B or IL-29
XX CC polypeptide having antiviral activity. One or more of the cysteine
XX CC residues were mutated to produce the proteins of the invention. The
XX CC invention may be useful for the development of a pharmaceutical
XX CC composition for the treatment of hepatitis B or C. The present sequence
XX CC is that of a novel IL variant protein of the invention.
XX CC
XX Sequence 181 AA;
XX SQ
Query Match 99.5%; Score 950; DB 9; Length 181;
Best Local Similarity 100.0%; Pred. No. 9.2e-91;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 GPVTSKPTTTGKGCHIGRFSLSPOELASFKKARDALAEESLKLKNWSCSSPVPPGNWDL 61
Db 1 GPVTSKPTTTGKGCHIGRFSLSPOELASFKKARDALAEESLKLKNWSCSSPVPPGNWDL 60
Qy 62 RLLQVRERPVVALEALALTTLKVLAAAGPALEDVLDQPLHTLHLHLSQLQACIQOPTAG 121
Db 61 RLLQVRERPVVALEALALTTLKVLAAAGPALEDVLDQPLHTLHLHLSQLQACIQOPTAG 120
Qy 122 PRPRGRHLHHLRLOEAPKESAGCLEASVTFNLFRLTRDLKYVADGNLSLRTSTHPES 181
Db 121 PRPRGRHLHHLRLOEAPKESAGCLEASVTFNLFRLTRDLKYVADGNLSLRTSTHPES 180
Qy 182 T 182
Db 181 T 181
RESULT 6
AD059978
ID AD059978 standard; protein; 182 AA.
XX AC
XX AD059978;
XX AC
XX 29-JUL-2004 (first entry)
XX DT
XX Met IL-29.
XX DE
XX interleukin; IL-28A; IL-28B; viral; infection; liver; inflammation;
XX KW viral load; anti-viral antibody; serological level;
XX KW alanine aminotransferase; histological improvement; hepatitis B;
XX KW hepatitis C; cytopaenia; leukocyte deficiency; neutropenia;
XX KW thrombocytopenia; anaemia; IL-29.
XX KW

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OS Homo sapiens.
XX WO2004037995-A2.
XX PN
XX 06-MAY-2004.
XX PD
XX 23-OCT-2003; 2003WO-US033628.
XX PF
XX 23-OCT-2002; 2002US-0420713P.
XX PR
XX 23-OCT-2002; 2002US-0420714P.
XX PR
XX 18-APR-2003; 2003US-0463939P.
XX PR
XX 18-APR-2003; 2003US-0463982P.
XX PR
XX (ZYMO ) ZYMOGENETICS INC.
XX PA
XX Klucher KM, Sivakumar PV, Kindsvogel WR, Henderson KE;
XX PI
XX WPI; 2004-365507/34.
XX DR N-PSDB; ADOS9977.
XX DR
XX Treating hepatitis B or hepatitis C virus infection comprises
XX PT administering to a mammal with a viral infection causing liver
XX PT inflammation, a polypeptide that is conjugated to a polyalkyl oxide
XX PT group.
XX PT
XX Claim 13; SEQ ID NO 38; 102pp; English.
XX PS
XX This sequence represents an interleukin Met-IL-29. This interleukin
XX CC protein may be used in the method of the invention for treating a viral
XX CC infection. The method comprises administering to a mammal with a viral
XX CC infection causing liver inflammation, an interleukin-based polypeptide,
XX CC where the viral infection level or liver inflammation is reduced. The
XX CC reduction in the viral infection level is measured as a decrease in viral
XX CC load, an increase in anti-viral antibodies, a decrease in serological
XX CC levels of alanine aminotransferase or histological improvement. The viral
XX CC infection is hepatitis B or C virus infection. The mammal has cytopaenia,
XX CC comprising leukocyte deficiency, neutropenia, thrombocytopenia or
XX CC anaemia. The interleukin polypeptide is interleukin 28 or 29, or a
XX CC variant of these. The method of the invention is useful in treating
XX CC hepatitis B or C virus infection.
XX CC
XX Sequence 182 AA;
XX SQ
Query Match 99.5%; Score 950; DB 8; Length 182;
Best Local Similarity 99.5%; Pred. No. 9.3e-91;
Matches 181; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 MGVPVTSKPTTTGKGCHIGRFSLSPOELASFKKARDALAEESLKLKNWSCSSPVPPGNWD 60
Db 1 MGVPVTSKPTTTGKGCHIGRFSLSPOELASFKKARDALAEESLKLKNWSCSSPVPPGNWD 60
Qy 61 LRLQVRERPVVALEALALTTLKVLAAAGPALEDVLDQPLHTLHLHLSQLQACIQOPTA 120
Db 61 LRLQVRERPVVALEALALTTLKVLAAAGPALEDVLDQPLHTLHLHLSQLQACIQOPTA 120
Qy 121 GPRPRGRHLHHLRLOEAPKESAGCLEASVTFNLFRLTRDLKYVADGNLSLRTSTHPE 180
Db 121 GPRPRGRHLHHLRLOEAPKESAGCLEASVTFNLFRLTRDLKYVADGNLSLRTSTHPE 180
Qy 181 ST 182
Db 181 ST 182
RESULT 7
ADY03588
ID ADY03588 standard; protein; 182 AA.
XX AC
XX ADY03588;
XX AC
XX 05-MAY-2005 (first entry)
XX DT
XX Human IL-29 mutant protein sequence SeqID15.
XX DE

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XX antiviral; pharmaceutical; hepatitis b virus infection;
 KW hepatitis c virus infection; mutant; mutein; IL-29.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX US2005037012-A1.
 XX 17-FEB-2005.

XX 09-AUG-2004; 2004US-00914772.
 XX 07-AUG-2003; 2003US-0493194P.
 PR 10-MAR-2004; 2004US-0551841P.
 PR 02-APR-2004; 2004US-0559142P.
 XX

(BRAD/) BRADY L J.
 PA (KLUC/) KLUCHER K M.
 PA (CHAN/) CHAN C.
 PA (DONG/) DONG D L.
 PA (LIUH/) LIU H Y.
 PA (SHEP/) SHEPPARD P O.
 PA (BUKO/) BUKOWSKI T R.

XX Brady LJ, Klucher KM, Chan C, Dong DL, Liu HY, Sheppard PO;
 PI Bukowski TR;
 XX

XX WPI; 2005-180368/19.
 DR N-PSDB; ADY03587.

XX Novel isolated Interleukin-28A, IL-28B or IL-29 polypeptide having anti-
 PT viral activity, useful for treating hepatitis B or hepatitis C
 PT infections.

XX Example 19; SEQ ID NO 15; 149pp; English.

XX This invention relates to a novel isolated IL-28A, IL-28B or IL-29
 CC polypeptide having antiviral activity. One or more of the cysteine
 CC residues were mutated to produce the proteins of the invention. The
 CC invention may be useful for the development of a pharmaceutical
 CC composition for the treatment of hepatitis B or C. The present sequence
 CC is that of a novel IL variant protein of the invention.

XX Sequence 182-AA;

Query Match 99.5%; Score 950; DB 9; Length 182;
 Best Local Similarity 99.5%; Pred. No. 9.3e-91;
 Matches 181; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGPVPTSKPTTGGKCHIGRFKSLSPQELASFKKARDALEESLKLKQWSSCSFVPGNWD 60
 DB 1 MGPVPTSKPTTGGKCHIGRFKSLSPQELASFKKARDALEESLKLKQWSSCSFVPGNWD 60
 QY 61 LRLQVRRPVALEAEALTLKYLEAAGPALEDVLDQPLHTLHILSLOQACIQOPTA 120
 DB 61 LRLQVRRPVALEAEALTLKYLEAAGPALEDVLDQPLHTLHILSLOQACIQOPTA 120
 QY 121 GPRPRGLHHLRLHLEAPKESAGCLEASVTNLFRLTLRDLKYVADGNLSLRTSTHPE 180
 DB 121 GPRPRGLHHLRLHLEAPKESAGCLEASVTNLFRLTLRDLKYVADGNLSLRTSTHPE 180
 QY 181 ST 182
 DB 181 ST 182

RESULT 8
 ADY03724
 ID ADY03724 standard; protein; 183 AA.
 XX
 AC ADY03724;
 XX

DT 05-MAY-2005 (first entry)

XX Human IL-29 mutant protein sequence SeqID151.

XX antiviral; pharmaceutical; hepatitis b virus infection;
 KW hepatitis c virus infection; mutant; mutein; IL-29.
 XX

OS Homo sapiens.
 OS Synthetic.

XX US2005037012-A1.

XX 17-FEB-2005.

XX 09-AUG-2004; 2004US-00914772.

PR 07-AUG-2003; 2003US-0493194P.

PR 10-MAR-2004; 2004US-0551841P.

PR 02-APR-2004; 2004US-0559142P.

XX (BRAD/) BRADY L J.

PA (KLUC/) KLUCHER K M.

PA (CHAN/) CHAN C.

PA (DONG/) DONG D L.

PA (LIUH/) LIU H Y.

PA (SHEP/) SHEPPARD P O.

PA (BUKO/) BUKOWSKI T R.

XX Brady LJ, Klucher KM, Chan C, Dong DL, Liu HY, Sheppard PO;
 PI Bukowski TR;
 XX

XX WPI; 2005-180368/19.

DR N-PSDB; ADY03723.

XX Novel isolated Interleukin-28A, IL-28B or IL-29 polypeptide having anti-
 PT viral activity, useful for treating hepatitis B or hepatitis C
 PT infections.

XX Claim 1; SEQ ID NO 151; 149pp; English.

XX This invention relates to a novel isolated IL-28A, IL-28B or IL-29
 CC polypeptide having antiviral activity. One or more of the cysteine
 CC residues were mutated to produce the proteins of the invention. The
 CC invention may be useful for the development of a pharmaceutical
 CC composition for the treatment of hepatitis B or C. The present sequence
 CC is that of a novel IL variant protein of the invention.

XX Sequence 183 AA;

Query Match 99.3%; Score 948; DB 9; Length 183;
 Best Local Similarity 98.9%; Pred. No. 1.5e-90;
 Matches 180; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGPVPTSKPTTGGKCHIGRFKSLSPQELASFKKARDALEESLKLKQWSSCSFVPGNWD 60
 DB 2 LGPVTSPKPTTGGKCHIGRFKSLSPQELASFKKARDALEESLKLKQWSSCSFVPGNWD 61
 QY 61 LRLQVRRPVALEAEALTLKYLEAAGPALEDVLDQPLHTLHILSLOQACIQOPTA 120
 DB 62 LRLQVRRPVALEAEALTLKYLEAAGPALEDVLDQPLHTLHILSLOQACIQOPTA 121
 QY 121 GPRPRGLHHLRLHLEAPKESAGCLEASVTNLFRLTLRDLKYVADGNLSLRTSTHPE 180
 DB 122 GPRPRGLHHLRLHLEAPKESAGCLEASVTNLFRLTLRDLKYVADGNLSLRTSTHPE 181
 QY 181 ST 182
 DB 182 ST 183

RESULT 9
 ADY03728
 ID ADY03728 standard; protein; 183 AA.

```
XX AC ADY03728;
XX DT 05-MAY-2005 (first entry)
XX DE Human IL-29 mutant protein sequence SeqID155.
XX KW antiviral; pharmaceutical; hepatitis b virus infection;
XX KW hepatitis c virus infection; mutant; mutein; IL-29.
XX OS Homo sapiens.
XX OS Synthetic.
XX PN US2005037012-A1.
XX PD 17-FEB-2005.
XX PF 09-AUG-2004; 2004US-00914772.
XX PR 07-AUG-2003; 2003US-0493194P.
XX PR 10-MAR-2004; 2004US-0551841P.
XX PR 02-APR-2004; 2004US-0559142P.
XX BRAD// BRADY L J.
XX PA (KLUC//) KLUCHER K M.
XX PA (CHAN//) CHAN C.
XX PA (DONG//) DONG D L.
XX PA (LIUH//) LIU H Y.
XX PA (SHEP//) SHEPPARD P O.
XX PA (BUKO//) BUKOWSKI T R.
XX PI Brady LJ, Klucher KM, Chan C, Dong DL, Liu HY, Sheppard PO;
XX PI Bukowski TR;
XX DR WPI; 2005-180368/19.
XX DR N-PSDB; ADY03727.
XX PT Novel isolated Interleukin-28A, IL-28B or IL-29 polypeptide having anti-
XX PT viral activity, useful for treating hepatitis B or hepatitis C
XX PT infections.
XX PS Claim 1; SEQ ID NO 155; 149pp; English.
XX CC This invention relates to a novel isolated IL-28A, IL-28B or IL-29
XX CC polypeptide having antiviral activity. One or more of the cysteine
XX CC residues were mutated to produce the proteins of the invention. The
XX CC invention may be useful for the development of a pharmaceutical
XX CC composition for the treatment of hepatitis B or C. The present sequence
XX CC is that of a novel IL variant protein of the invention.
XX SQ Sequence 183 AA;
Query Match 99.2%; Score 947; DB 9; Length 183;
Best Local Similarity 98.9%; Pred. No. 1.9e-90;
Matches 180; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 MGPVPTSKPTTGGKCHIGRFKSLSPQELASFKKARDALAEESLKLKNWSCSSPVFPGNWD 60
DB 2 IGPVPTSKPTTGGKCHIGRFKSLSPQELASFKKARDALAEESLKLKNWSCSSPVFPGNWD 61
QY 61 LRLQVRRPVALEAELALTLKVLEAAAGPALEDVLDQPLHTLHILSLQACIQPQTA 120
DB 62 LRLQVRRPVALEAELALTLKVLEAAAGPALEDVLDQPLHTLHILSLQACIQPQTA 121
QY 121 GPRGRLLHWHRLQEQAPKESAGCLEASVTFNLFRLITRDLKVVADGNLSLRTSTHPE 180
DB 122 GPRGRLLHWHRLQEQAPKESAGCLEASVTFNLFRLITRDLKVVADGNLSLRTSTHPE 181
QY 181 ST 182
DB 182 ST 183
```

```
RESULT 10
ADY03613
ID ADY03613 standard; protein; 181 AA.
XX AC ADY03613;
XX DT 05-MAY-2005 (first entry)
XX DE Human IL-28A mutant protein sequence SeqID40.
XX KW antiviral; pharmaceutical; hepatitis b virus infection;
XX KW hepatitis c virus infection; mutant; mutein; IL-28A.
XX OS Homo sapiens.
XX OS Synthetic.
XX PN US2005037012-A1.
XX PD 17-FEB-2005.
XX PF 09-AUG-2004; 2004US-00914772.
XX PR 07-AUG-2003; 2003US-0493194P.
XX PR 10-MAR-2004; 2004US-0551841P.
XX PR 02-APR-2004; 2004US-0559142P.
XX BRAD// BRADY L J.
XX PA (KLUC//) KLUCHER K M.
XX PA (CHAN//) CHAN C.
XX PA (DONG//) DONG D L.
XX PA (LIUH//) LIU H Y.
XX PA (SHEP//) SHEPPARD P O.
XX PA (BUKO//) BUKOWSKI T R.
XX PI Brady LJ, Klucher KM, Chan C, Dong DL, Liu HY, Sheppard PO;
XX PI Bukowski TR;
XX DR WPI; 2005-180368/19.
XX DR N-PSDB; ADY03607.
XX PT Novel isolated Interleukin-28A, IL-28B or IL-29 polypeptide having anti-
XX PT viral activity, useful for treating hepatitis B or hepatitis C
XX PT infections.
XX PS Claim 1; SEQ ID NO 40; 149pp; English.
XX CC This invention relates to a novel isolated IL-28A, IL-28B or IL-29
XX CC polypeptide having antiviral activity. One or more of the cysteine
XX CC residues were mutated to produce the proteins of the invention. The
XX CC invention may be useful for the development of a pharmaceutical
XX CC composition for the treatment of hepatitis B or C. The present sequence
XX CC is that of a novel IL variant protein of the invention.
XX SQ Sequence 181 AA;
Query Match 99.1%; Score 946; DB 9; Length 181;
Best Local Similarity 99.4%; Pred. No. 2.4e-90;
Matches 180; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 GPVPTSKPTTGGKCHIGRFKSLSPQELASFKKARDALAEESLKLKNWSCSSPVFPGNWDL 61
DB 1 GPVPTSKPTTGGKCHIGRFKSLSPQELASFKKARDALAEESLKLKNWSCSSPVFPGNWDL 60
QY 62 LRLQVRRPVALEAELALTLKVLEAAAGPALEDVLDQPLHTLHILSLQACIQPQTAG 121
DB 61 LRLQVRRPVALEAELALTLKVLEAAAGPALEDVLDQPLHTLHILSLQACIQPQTAG 120
QY 122 PRPRGRLLHWHRLQEQAPKESAGCLEASVTFNLFRLITRDLKVVADGNLSLRTSTHPE 181
DB 121 PRPRGRLLHWHRLQEQAPKESAGCLEASVTFNLFRLITRDLKVVADGNLSLRTSTHPE 180
QY 182 T 182
```

```
Db          181 T 181

RESULT 11
ADY03658
ID ADY03658 standard; protein; 182 AA.
XX
AC ADY03658;
XX
DT 05-MAY-2005 (first entry)
XX
DE Human IL-29 mutant protein sequence SeqID85.
XX
KW antiviral; pharmaceutical; hepatitis b virus infection;
KW hepatitis c virus infection; mutant; mutein; IL-29.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN US2005037012-A1.
XX
PD 17-FEB-2005.
XX
PF 09-AUG-2004; 2004US-00914772.
XX
PR 07-AUG-2003; 2003US-0493194P.
PR 10-MAR-2004; 2004US-0551841P.
PR 02-APR-2004; 2004US-0559142P.
XX
PA (BRAD//) BRADY L J.
PA (KLUC//) KLUCHER K M.
PA (CHAN//) CHAN C.
PA (DONG//) DONG D L.
PA (LIUH//) LIU H Y.
PA (SHEP//) SHEPPARD P O.
PA (BUKO//) BUKOWSKI T R.
XX
PI Brady LJ, Klucher KM, Chan C, Dong DL, Liu HY, Sheppard PO;
PI Bukowski TR;
XX
WPI; 2005-180368/19.
N-PSDB; ADY03657.
XX
Novel isolated Interleukin-28A, IL-28B or IL-29 polypeptide having anti-
viral activity, useful for treating hepatitis B or hepatitis C
infections.
XX
Claim 1; SEQ ID NO 85; 149pp; English.
XX
This invention relates to a novel isolated IL-28A, IL-28B or IL-29
polypeptide having antiviral activity. One or more of the cysteine
residues were mutated to produce the proteins of the invention. The
invention may be useful for the development of a pharmaceutical.
XX
composition for the treatment of hepatitis B or C. The present sequence
is that of a novel IL variant protein of the invention.
XX
SQ Sequence 182 AA;

Query Match          99.1%; Score 946; DB 9; Length 182;
Best Local Similarity 98.9%; Pred. No. 2.4e-90;
Matches 180; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy          1 MGPVTSKPTTTGKGCHIGRFKSLSPQELASFKKARDALAEESLKLKNWSCSPVPFGNWD 60
Db          1 MGPVTSKPTTTGKGCHIGRFKSLSPQELASFKKARDALAEESLKLKNWSCSPVPFGNWD 60
Qy          61 LRLQVRERPVAAEALTLKVLAAAGPALEDVLDQPLHTLHHLSQLQACIQPQTA 120
Db          61 LRLQVRERPVAAEALTLKVLAAAGPALEDVLDQPLHTLHHLSQLQACIQPQTA 120
Qy          121 GPRGRHLHHLRLOEAPKESAGCLEASVTFNLFRLTLTRDLKYVADGNLSLTSTHPE 180
Db          121 GPRGRHLHHLRLOEAPKESAGCLEASVTFNLFRLTLTRDLKYVADGNLSLTSTHPE 180

Qy          181 ST 182
Db          181 ST 182

RESULT 12
ADY03734
ID ADY03734 standard; protein; 185 AA.
XX
AC ADY03734;
XX
DT 05-MAY-2005 (first entry)
XX
DE Human IL-29 mutant protein sequence SeqID161.
XX
KW antiviral; pharmaceutical; hepatitis b virus infection;
KW hepatitis c virus infection; mutant; mutein; IL-29.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN US2005037012-A1.
XX
PD 17-FEB-2005.
XX
PF 09-AUG-2004; 2004US-00914772.
XX
PR 07-AUG-2003; 2003US-0493194P.
PR 10-MAR-2004; 2004US-0551841P.
PR 02-APR-2004; 2004US-0559142P.
XX
PA (BRAD//) BRADY L J.
PA (KLUC//) KLUCHER K M.
PA (CHAN//) CHAN C.
PA (DONG//) DONG D L.
PA (LIUH//) LIU H Y.
PA (SHEP//) SHEPPARD P O.
PA (BUKO//) BUKOWSKI T R.
XX
PI Brady LJ, Klucher KM, Chan C, Dong DL, Liu HY, Sheppard PO;
PI Bukowski TR;
XX
WPI; 2005-180368/19.
N-PSDB; ADY03733.
XX
Novel isolated Interleukin-28A, IL-28B or IL-29 polypeptide having anti-
viral activity, useful for treating hepatitis B or hepatitis C
infections.
XX
Claim 1; SEQ ID NO 161; 149pp; English.
XX
This invention relates to a novel isolated IL-28A, IL-28B or IL-29
polypeptide having antiviral activity. One or more of the cysteine
residues were mutated to produce the proteins of the invention. The
invention may be useful for the development of a pharmaceutical.
XX
composition for the treatment of hepatitis B or C. The present sequence
is that of a novel IL variant protein of the invention.
XX
SQ Sequence 185 AA;

Query Match          99.1%; Score 946; DB 9; Length 185;
Best Local Similarity 99.4%; Pred. No. 2.5e-90;
Matches 180; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy          2 GPVPTSPTTTGKGCHIGRFKSLSPQELASFKKARDALAEESLKLKNWSCSPVPFGNWDL 61
Db          5 GPVPTSPTTTGKGCHIGRFKSLSPQELASFKKARDALAEESLKLKNWSCSPVPFGNWDL 64
Qy          62 RLQVRERPVAAEALTLKVLAAAGPALEDVLDQPLHTLHHLSQLQACIQPQTAG 121
Db          65 RLQVRERPVAAEALTLKVLAAAGPALEDVLDQPLHTLHHLSQLQACIQPQTAG 124
```

QY 122 PRPRGRHLHRLHRLQAPKESAGCLEASVTNLFRLTRDLKYVADGNLSLRTSTHPE 181
 DB 125 PRPRGRHLHRLHRLQAPKESAGCLEASVTNLFRLTRDLKYVADGNLSLRTSTHPE 184
 QY 182 T 182
 DB 185 T 185

RESULT 13
 ADY03662
 ID ADY03662 standard; protein; 182 AA.
 XX
 AC ADY03662;
 DT 05-MAY-2005 (first entry)
 XX
 DE Human IL-29 mutant protein sequence SeqID89.
 XX
 KW antiviral; pharmaceutical; hepatitis b virus infection;
 KW hepatitis c virus infection; mutant; mutein; IL-29.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN US2005037012-A1.
 XX
 PD 17-FEB-2005.
 XX
 PF 09-AUG-2004; 2004US-00914772.
 XX
 PR 07-AUG-2003; 2003US-0493194P.
 PR 10-MAR-2004; 2004US-0551841P.
 PR 02-APR-2004; 2004US-0559142P.
 XX
 PA (BRAD//) BRADY L J.
 PA (KLUC//) KLUCHER K M.
 PA (CHAN//) CHAN C.
 PA (DONG//) DONG D L.
 PA (LIUH//) LIU H Y.
 PA (SHEP//) SHEPPARD P O.
 PA (BUKO//) BUKOWSKI T R.
 XX
 PI Brady LJ, Klucher KM, Chan C, Dong DL, Liu HY, Sheppard PO;
 PI Bukowski TR;
 PI
 DR WPI; 2005-180368/19.
 DR N-PSDB; ADY03661.
 XX
 PT Novel isolated interleukin-28A, IL-28B or IL-29 polypeptide having anti-viral activity, useful for treating hepatitis B or hepatitis C infections.
 PT
 XX
 PS Claim 1; SEQ ID NO 89; 149pp; English.
 XX
 CC This invention relates to a novel isolated IL-28A, IL-28B or IL-29 polypeptide having antiviral activity. One or more of the cysteine residues were mutated to produce the proteins of the invention. The invention may be useful for the development of a pharmaceutical composition for the treatment of hepatitis B or C. The present sequence is that of a novel IL variant protein of the invention.
 CC
 XX
 SQ Sequence 182 AA;
 Query Match 99.0%; Score 945; DB 9; Length 182;
 Best Local Similarity 98.9%; Pred. No. 3.1e-90;
 Matches 180; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MGPVPTSKPTTGKCHIGRFSLSPOELASFKKARDALBESLKLKWSGSPVPPGNWD 60
 DB 1 MGPVPTSKPTTGKCHIGRFSLSPOELASFKKARDALBESLKLKWSGSPVPPGNWD 60
 QY 61 LRLQVRRPVALEALATLKVLEAAAGPALEDVLDQPLTLHLHLSQLQACIQPPTA 120

DB 61 LRLQVRRPVALEALATLKVLEAAAGPALEDVLDQPLTLHLHLSQLQACIQPPTA 120
 QY 121 GPRPRGRHLHRLHRLQAPKESAGCLEASVTNLFRLTRDLKYVADGNLSLRTSTHPE 180
 DB 121 GPRPRGRHLHRLHRLQAPKESAGCLEASVTNLFRLTRDLKYVADGNLSLRTSTHPE 180
 QY 181 ST 182
 DB 181 ST 182

RESULT 14
 AAE18311
 ID AAE18311 standard; protein; 200 AA.
 XX
 AC AAE18311;
 XX
 DT 07-MAY-2002 (first entry)
 XX
 DE Human Zcyto21 consensus protein.
 XX
 KW Human; interferon like protein; IFN; genetic disease; transgenic animal; cancer; immune regulation; rheumatoid arthritis; multiple sclerosis; myasthenia gravis; systemic lupus erythematosus; diabetes; inflammation; tumour; viral infection; graft rejection; human immuno deficiency virus; HIV; behavioural disorder; reproductive disorder; vaccine adjuvant;
 KW sepsis; cytostatic; neuroprotective; dermatological; immunosuppressive;
 KW Zcyto21 protein; chromosome 19q13.13.
 XX
 OS Homo sapiens.
 XX
 PN WO200202627-A2.
 XX
 PD 10-JAN-2002.
 XX
 PF 29-JUN-2001; 2001WO-US021087.
 XX
 PR 30-JUN-2000; 2000US-0215446P.
 PR 20-APR-2001; 2001US-0285424P.
 XX
 PA (ZYMO) ZYMOGENETICS INC.
 XX
 PI Sheppard PO, Presnell SR, Fox BA, Gilbert T, Haldeman BA;
 PI Grant FJ;
 PI
 DR WPI; 2002-171640/22.
 DR N-PSDB; AAD29146.
 XX
 PT New polypeptide Zcyto21, which is related to interferon, is useful e.g. for treating viral infection and immunological disease.
 PT
 XX
 PS Disclosure; Page 75; 82pp; English.
 XX
 CC The patent discloses novel polynucleotide and polypeptide molecules for Zcyto21, an interferon (IFN) like protein which is most closely related to INF-alpha. Zcyto21 DNAs are useful for detecting the corresponding genes and its mutants, e.g. for diagnosis of genetic diseases and cancer or for detecting chromosome 19 deletions and translocations associated with diseases. They are useful for preparing transgenic animals used to study the Zcyto21 gene and protein and as antisense inhibitors. Zcyto21 sequences and their inhibitors are useful for treating diseases that require immune regulation (e.g. rheumatoid arthritis, multiple sclerosis, myasthenia gravis, systemic lupus erythematosus and diabetes), tumours, inflammation (e.g. arthritis or sepsis), viral infections (e.g. human immune deficiency viruses (HIV) and papilloma viruses), graft rejection, behavioural and reproductive disorders. They are also used as vaccine adjuvants. They can also be used to identify specific inhibitors and receptors. The present sequence is human Zcyto21 consensus protein.
 CC
 XX Zcyto21 gene is located on chromosome 19q13.13
 SQ Sequence 200 AA;

Query Match 99.0%; Score 945; DB 5; Length 200;
Best Local Similarity 99.4%; Pred. No. 3.5e-90;
Matches 180; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GPVPTSKPTTTGKGCHIGRFKSLSPQELASFKKARDALAEESLKLKNWSCSPVPPGNWDL 61
DB 20 GPVPTSKPTTTGKGCHIGRFKSLSPQELASFKKARDALAEESLKLKNWSCSPVPPGNWDL 79

QY 62 RLQVRERPVVALEAELALTLKYLEAAGPALEDVLDQPLHTLHHILSLOLQACIQOPTAG 121
DB 80 RLQVRERPVVALEAELALTLKYLEAAGPALEDVLDQPLHTLHHILSLOLQACIQOPTAG 139

QY 122 PRPRGRHLHHLRLQEAAPKESAGCLEASVTFNLFRLTLRDLKYVADGNLSLRTSTHPES 181
DB 140 PRPRGRHLHHLRLQEAAPKESAGCLEASVTFNLFRLTLRDLKYVADGNLSLRTSTHPES 199

QY 182 T 182
DB 200 T 200

RESULT 15
AAE18310
ID AAE18310 standard; protein; 200 AA.
AC AAE18310;
XX 07-MAY-2002 (first entry)
XX Human Zcyto21 allelic variant protein.
XX Human; interferon like protein; IFN; genetic disease; transgenic animal;
KW cancer; immune regulation; rheumatoid arthritis; multiple sclerosis;
KW myasthenia gravis; systemic lupus erythematosus; diabetes; inflammation;
KW tumour; viral infection; graft rejection; human immuno deficiency virus;
KW HIV; behavioural disorder; reproductive disorder; vaccine adjuvant;
KW sepsis; cytostatic; neuroprotective; dermatological; immunosuppressive;
KW Zcyto21 protein.
XX
XX Homo sapiens.
XX WO200202627-A2.
XX 10-JAN-2002.
XX 29-JUN-2001; 2001WO-US021087.
XX 30-JUN-2000; 2000US-0215446P.
XX 20-APR-2001; 2001US-0285424P.
XX (ZYMO) ZYMOGENETICS INC.
XX Sheppard PO, Presnell SR, Fox BA, Gilbert T, Haldeman BA;
PI Grant PJ;
XX WPI; 2002-171640/22.
XX N-PSDB; AAD29145.
XX New polypeptide Zcyto21, which is related to interferon, is useful e.g.
XX for treating viral infection and immunological disease.
XX Disclosure; Page 72-73; 82pp; English.
XX The patent discloses novel polynucleotide and polypeptide molecules for
XX Zcyto21, an interferon (IFN) like protein which is most closely related
XX to INF-alpha. Zcyto21 DNAs are useful for detecting the corresponding
XX genes and its mutants, e.g. for diagnosis of genetic diseases and cancer
XX or for detecting chromosome 19 deletions and translocations associated
XX with diseases. They are useful for preparing transgenic animals used to
XX study the Zcyto21 gene and protein and as antisense inhibitors. Zcyto21
XX sequences and their inhibitors are useful for treating diseases that
XX require immune regulation (e.g. rheumatoid arthritis, multiple sclerosis,
XX myasthenia gravis, systemic lupus erythematosus and diabetes), tumours,

CC inflammation (e.g. arthritis or sepsis), viral infections (e.g., human
CC immune deficiency viruses (HIV) and papilloma viruses), graft rejection,
CC behavioural and reproductive disorders. They are also used as vaccine
CC adjuvants. They can also be used to identify specific inhibitors and
CC receptors. The present sequence is human Zcyto21 allelic variant protein
XX
SQ Sequence 200 AA;
Query Match 99.0%; Score 945; DB 5; Length 200;
Best Local Similarity 99.4%; Pred. No. 3.5e-90;
Matches 180; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GPVPTSKPTTTGKGCHIGRFKSLSPQELASFKKARDALAEESLKLKNWSCSPVPPGNWDL 61
DB 20 GPVPTSKPTTTGKGCHIGRFKSLSPQELASFKKARDALAEESLKLKNWSCSPVPPGNWDL 79

QY 62 RLQVRERPVVALEAELALTLKYLEAAGPALEDVLDQPLHTLHHILSLOLQACIQOPTAG 121
DB 80 RLQVRERPVVALEAELALTLKYLEAAGPALEDVLDQPLHTLHHILSLOLQACIQOPTAG 139

QY 122 PRPRGRHLHHLRLQEAAPKESAGCLEASVTFNLFRLTLRDLKYVADGNLSLRTSTHPES 181
DB 140 PRPRGRHLHHLRLQEAAPKESAGCLEASVTFNLFRLTLRDLKYVADGNLSLRTSTHPES 199

QY 182 T 182
DB 200 T 200

Search completed: December 29, 2005, 13:55:15
Job time : 188 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 29, 2005, 13:47:27 ; Search time 46 Seconds
(without alignments)
327.108 Million cell updates/sec

Title: US-10-691-923-34
Perfect score: 955
Sequence: 1 MGPVTSKPTTGGCHIGR.....LKYVADGNLSLRTSTHPST 182

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgn2_6/ptodata/1/iaa/5 COMB.pep.*

2: /cgn2_6/ptodata/1/iaa/6 COMB.pep.*

3: /cgn2_6/ptodata/1/iaa/H COMB.pep.*

4: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pep.*

5: /cgn2_6/ptodata/1/iaa/RE COMB.pep.*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	945	99.0	200	2	US-09-895-834-5
2	945	99.0	200	2	US-09-895-834-7
3	940	98.4	200	2	US-09-893-737-268
4	940	98.4	200	2	US-09-895-834-2
5	940	98.4	203	2	US-09-895-834-12
6	940	98.4	219	2	US-09-895-834-9
7	83	8.7	567	2	US-09-538-092-1365
8	82	8.6	315	2	US-09-370-398-6
9	82	8.6	315	2	US-10-090-190-6
10	82	8.6	315	2	US-10-082-902-6
11	82	8.6	899	2	US-09-538-092-27
12	81.5	8.5	1228	2	US-09-252-991A-17764
13	81	8.5	164	2	US-10-104-047-3099
14	80	8.4	563	1	PCT-US061-636-2
15	80	8.4	563	4	PCT-US94-05268-2
16	79.5	8.3	315	2	US-08-965-9038-8
17	79.5	8.3	315	2	US-09-370-398-3
18	79.5	8.3	315	2	US-10-090-190-3
19	79.5	8.3	315	2	US-10-082-902-3
20	79	8.3	495	2	US-09-712-362-181
21	79	8.3	903	2	US-09-758-007-1
22	79	8.3	1114	2	US-09-637-145-4
23	78.5	8.2	378	2	US-09-724-797-40
24	78.5	8.2	780	2	US-09-771-161A-144
25	78.5	8.2	942	2	US-08-685-852-3
26	78.5	8.2	942	2	US-09-771-161A-235
27	78.5	8.2	942	2	US-09-771-161A-236

28	77.5	8.1	180	2	US-09-252-991A-18500	Sequence 18500, A
29	77	8.1	198	2	US-09-489-039A-9420	Sequence 9420, Ap
30	77	8.1	542	2	US-09-252-991A-32139	Sequence 32139, A
31	76	8.0	302	2	US-09-489-039A-7999	Sequence 7999, Ap
32	76	8.0	560	2	US-09-252-991A-27301	Sequence 27301, A
33	75.5	7.9	654	2	US-09-949-002-389	Sequence 389, App
34	75.5	7.9	683	2	US-09-949-002-424	Sequence 424, App
35	75	7.9	229	2	US-09-270-767-31836	Sequence 31836, A
36	75	7.9	640	2	US-09-487-558B-84	Sequence 94, Appl
37	74.5	7.8	227	2	US-09-949-016-10420	Sequence 10420, A
38	74.5	7.8	373	2	US-09-919-497-53	Sequence 53, Appl
39	74.5	7.8	384	2	US-09-949-016-11663	Sequence 11663, A
40	74.5	7.8	767	2	US-09-949-016-6167	Sequence 6167, Ap
41	74.5	7.8	789	2	US-09-949-016-9432	Sequence 9432, Ap
42	74.5	7.8	908	2	US-09-949-016-8542	Sequence 8542, Ap
43	74.5	7.8	1403	2	US-09-262-537-6	Sequence 6, Appl
44	74.5	7.8	1531	2	US-09-949-016-6740	Sequence 6740, Ap
45	74	7.7	653	2	US-09-252-991A-27553	Sequence 27553, A

ALIGNMENTS

RESULT 1

US-09-895-834-5

; Sequence 5, Application US/09895834

; Patent No. 6927040

; GENERAL INFORMATION:

; APPLICANT: Sheppard, Paul O.

; APPLICANT: Presnell, Scott R.

; APPLICANT: Fox, Brian A.

; APPLICANT: Gilbert, Teresa

; APPLICANT: Haldeman, Betty A.

; APPLICANT: Grant, Francis J.

; TITLE OF INVENTION: INTERFERON-LIKE PROTEIN ZCYTO21

; FILE REFERENCE: 01-18

; CURRENT APPLICATION NUMBER: US/09/895,834

; CURRENT FILING DATE: 2001-06-29

; PRIOR APPLICATION NUMBER: 60/285,424

; PRIOR FILING DATE: 2001-04-20

; PRIOR APPLICATION NUMBER: 60/215,446

; PRIOR FILING DATE: 2000-06-30

; NUMBER OF SEQ ID NOS: 16

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 5

; LENGTH: 200

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-895-834-5

Query Match 99.0%; Score 945; DB 2; Length 200;

Best Local Similarity 99.4%; Pred. No. 5.3e-99;

Matches 180; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	2	GPVPTSKPTTGGCHIGRFSKLSPOELASFKKARDALEESLKNWSSSPVFFGNWDL	61
Db	20	GPVTSKPTTGGCHIGRFSKLSPOELASFKKARDALEESLKNWSSSPVFFGNWDL	79
QY	62	RLQVRPVALEAEALTLTKVLEAAGPALEDVLDQPLHTLHLSQLQACIQOPTAG	121
Db	80	RLQVRPVALEAEALTLTKVLEAAGPALEDVLDQPLHTLHLSQLQACIQOPTAG	139
QY	122	PRPGRHLHRLHQEAPKKSAGCLEASVTNLFRLTRDLKYVADGNLSLRTSTHPES	181
Db	140	PRPGRHLHRLHQEAPKKSAGCLEASVTNLFRLTRDLKYVADGNLSLRTSTHPES	199
QY	182	T 182	
Db	200	T 200	

RESULT 2

US-09-895-834-7


```
; Sequence 7, Application US/09895834
; Patent No. 6927040
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Fox, Brian A.
; APPLICANT: Gilbert, Teresa
; APPLICANT: Haldeman, Betty A.
; APPLICANT: Grant, Francis J.
; TITLE OF INVENTION: INTERFERON-LIKE PROTEIN ZCYTO21
; FILE REFERENCE: 01-18
; CURRENT APPLICATION NUMBER: US/09/895,834
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 60/285,424
; PRIOR FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: 60/215,446
; PRIOR FILING DATE: 2000-06-30
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 200
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-895-834-7

Query Match      99.0%; Score 945; DB 2; Length 200;
Best Local Similarity 99.4%; Pred. No. 5.3e-99;
Matches 180; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      2 GPVPTSKPTTGGCHIGRFKSLSPQELASFKKARDALAEESLKLKNWSCSSPVFFGNWDL 61
Db      20 GPVPTSKPTTGGCHIGRFKSLSPQELASFKKARDALAEESLKLKNWSCSSPVFFGNWDL 79

Qy      62 RLLQVRERPVVALEAEALTLTKVLEAAAGPALEDVLDQPLHTLHHLSQLQACIQOPTAG 121
Db      80 RLLQVRERPVVALEAEALTLTKVLEAAAGPALEDVLDQPLHTLHHLSQLQACIQOPTAG 139

Qy      122 PRPRGRLLHHLRLQEAAPKESAGCLEASVTNLFRLTRDLKYVADGNLSLRTSTHPES 181
Db      140 PRPRGRLLHHLRLQEAAPKESAGCLEASVTNLFRLTRDLKYVADGNLSLRTSTHPES 199

Qy      182 T 182
Db      200 T 200

RESULT 4
US-09-895-834-2
; Sequence 2, Application US/09895834
; Patent No. 6927040
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Fox, Brian A.
; APPLICANT: Gilbert, Teresa
; APPLICANT: Haldeman, Betty A.
; APPLICANT: Grant, Francis J.
; TITLE OF INVENTION: INTERFERON-LIKE PROTEIN ZCYTO21
; FILE REFERENCE: 01-18
; CURRENT APPLICATION NUMBER: US/09/895,834
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 60/285,424
; PRIOR FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: 60/215,446
; PRIOR FILING DATE: 2000-06-30
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 200
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-895-834-2

Query Match      98.4%; Score 940; DB 2; Length 200;
Best Local Similarity 98.9%; Pred. No. 1.9e-98;
Matches 179; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      2 GPVPTSKPTTGGCHIGRFKSLSPQELASFKKARDALAEESLKLKNWSCSSPVFFGNWDL 61
Db      20 GPVPTSKPTTGGCHIGRFKSLSPQELASFKKARDALAEESLKLKNWSCSSPVFFGNWDL 79

Qy      62 RLLQVRERPVVALEAEALTLTKVLEAAAGPALEDVLDQPLHTLHHLSQLQACIQOPTAG 121
Db      80 RLLQVRERPVVALEAEALTLTKVLEAAAGPALEDVLDQPLHTLHHLSQLQACIQOPTAG 139

Qy      122 PRPRGRLLHHLRLQEAAPKESAGCLEASVTNLFRLTRDLKYVADGNLSLRTSTHPES 181
Db      140 PRPRGRLLHHLRLQEAAPKESAGCLEASVTNLFRLTRDLKYVADGNLSLRTSTHPES 199

Qy      182 T 182
Db      200 T 200

RESULT 5
US-09-895-834-12
; Sequence 12, Application US/09895834
; Patent No. 6927040
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Fox, Brian A.
; APPLICANT: Gilbert, Teresa
; APPLICANT: Haldeman, Betty A.
```

```
; APPLICANT: Grant, Francis J.
; FILE OF INVENTION: INTERFERON-LIKE PROTEIN ZCVT021
; CURRENT APPLICATION NUMBER: US/09/895,834
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 60/285,424
; PRIOR FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: 60/215,446
; PRIOR FILING DATE: 2000-06-30
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 203
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-895-834-12

Query Match      98.4%; Score 940; DB 2; Length 203;
Best Local Similarity 98.9%; Pred. No. 2e-98;
Matches 179; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      2  GVPVTSKPTTGKGCHIGRFKLSPOELASFKKARDALLESKLKNWSCSSPVFPGNWDL 61
Db      23  GVPVTSKPTTGKGCHIGRFKLSPOELASFKKARDALLESKLKNWSCSSPVFPGNWDL 82

QY      62  RLLQVRERPVVALEALTLKYLEAAAGPALEDVLDQPLHTLHHLSQLQACIQOPTAG 121
Db      83  RLLQVRERPVVALEALTLKYLEAAAGPALEDVLDQPLHTLHHLSQLQACIQOPTAG 142

QY      122  PRPRGRLLHHLRLQEPAPKESAGCLEASVTNLFRLTRDLKYVADGNLSLRTSTHPES 181
Db      143  PRPRGRLLHHLRLQEPAPKESAGCLEASVTNLFRLTRDLKYVADGNLSLRTSTHPES 202

QY      182  T 182
Db      203  T 203

RESULT 6
US-09-895-834-9
; Sequence 9, Application US/09895834
; Patent No. 6927040
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Preenell, Scott R.
; APPLICANT: Fox, Brian A.
; APPLICANT: Gilbert, Teresa
; APPLICANT: Haldeman, Betty A.
; APPLICANT: Grant, Francis J.
; TITLE OF INVENTION: INTERFERON-LIKE PROTEIN ZCVT021
; FILE REFERENCE: 01-18
; CURRENT APPLICATION NUMBER: US/09/895,834
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 60/285,424
; PRIOR FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: 60/215,446
; PRIOR FILING DATE: 2000-06-30
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-895-834-9

Query Match      98.4%; Score 940; DB 2; Length 219;
Best Local Similarity 98.9%; Pred. No. 2.2e-98;
Matches 179; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      2  GVPVTSKPTTGKGCHIGRFKLSPOELASFKKARDALLESKLKNWSCSSPVFPGNWDL 61
Db      39  GVPVTSKPTTGKGCHIGRFKLSPOELASFKKARDALLESKLKNWSCSSPVFPGNWDL 98

; APPLICANT: Grant, Francis J.
; FILE OF INVENTION: INTERFERON-LIKE PROTEIN ZCVT021
; CURRENT APPLICATION NUMBER: US/09/895,834
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 60/285,424
; PRIOR FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: 60/215,446
; PRIOR FILING DATE: 2000-06-30
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 203
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-895-834-12

Query Match      98.4%; Score 940; DB 2; Length 203;
Best Local Similarity 98.9%; Pred. No. 2e-98;
Matches 179; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      2  GVPVTSKPTTGKGCHIGRFKLSPOELASFKKARDALLESKLKNWSCSSPVFPGNWDL 61
Db      23  GVPVTSKPTTGKGCHIGRFKLSPOELASFKKARDALLESKLKNWSCSSPVFPGNWDL 82

QY      62  RLLQVRERPVVALEALTLKYLEAAAGPALEDVLDQPLHTLHHLSQLQACIQOPTAG 121
Db      83  RLLQVRERPVVALEALTLKYLEAAAGPALEDVLDQPLHTLHHLSQLQACIQOPTAG 142

QY      122  PRPRGRLLHHLRLQEPAPKESAGCLEASVTNLFRLTRDLKYVADGNLSLRTSTHPES 181
Db      143  PRPRGRLLHHLRLQEPAPKESAGCLEASVTNLFRLTRDLKYVADGNLSLRTSTHPES 202

QY      182  T 182
Db      203  T 203

RESULT 7
US-09-538-092-1365
; Sequence 1365, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Giot, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CurapatSeqformat Version 0.9
; SEQ ID NO 1365
; LENGTH: 567
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number Q92696
US-09-538-092-1365

Query Match      8.7%; Score 83; DB 2; Length 567;
Best Local Similarity 25.6%; Pred. No. 1.4;
Matches 50; Conservative 16; Mismatches 59; Indels 70; Gaps 9;

QY      25  SPOELASFKKAR-DALLESKLKNWSCSSPVFPGNWDLRLLOVRERPVVA-LEALALTLK 82
Db      81  SPEELALVKAEELGFLESLRV-----NPKSYGTWHRCWLGLRLEPNWTRLELCAR 134

QY      83  VLE-----AAAGPALEDVLDQPLHTLH-----HLSQLQACIQOPQ 117
Db      135  FLEVDERNFHCWYRRFVATQAAPAEALFTDSLITRNFSNYSWYHVRSCLLPQLHPQ 194

QY      118  PTAGPRPRGRLL-----HHWHLRLQEPAPKESACCL--- 147
Db      195  PDSG--PQRLPEDVLLKELELVQNVAFTDPNDQSAWFYHRL--LGRADPQDALRCLHV 250

QY      148  ---EASVTNLFRL 159
Db      251  SRDEACTVTSFRPL 265

RESULT 8
US-09-370-398-6
; Sequence 6, Application US/09370398
; Patent No. 6423682
; GENERAL INFORMATION:
; APPLICANT: Ballinger, Dennis G.
; APPLICANT: Montgomery, Julie R.
; TITLE OF INVENTION: Growth Factor Antagonist Materials and Methods
; FILE REFERENCE: 28110/35878
; CURRENT APPLICATION NUMBER: US/09/370,398
; CURRENT FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 13
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; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 17764
; LENGTH: 1228
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
; NAME/KEY: UNSURE
; FEATURE:
; LOCATION: (17)
; OTHER INFORMATION: Identity of amino acid at the above locations are unknown.
US-09-252-991A-17764

Query Match      8.5%; Score 81.5; DB 2; Length 1228;
Best Local Similarity 33.0%; Pred. No. 5.9;
Matches 32; Conservative 5; Mismatches 33; Indels 27; Gaps 5;

QY 56 PGNWDLRL-----LQVRPVPVLEAEALTLKVLAAAGPALEDVLDQPLHTLHIL 107
Db 738 PGRADLRPRADRRHHPLQRRSPVARRS-----GHARGQA--PVLDPGHSAAH--- 784

QY 108 SOLQACIQQP-----TAGPRPRGRLLHHLHRLHRLQEPK 140
Db 785 --LRAAVPQPGHRADQDPDARRRLRHRLHRLHRLPR 819

RESULT 13
US-10-104-047-3099
; Sequence 3099, Application US/10104047
; Patent No. 6943241
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. 6943241el full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 3099
; LENGTH: 164
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-104-047-3099

Query Match      8.5%; Score 81; DB 2; Length 164;
Best Local Similarity 24.3%; Pred. No. 0.41;
Matches 41; Conservative 21; Mismatches 59; Indels 48; Gaps 9;

QY 1 MGPVPPTSKPTTGKGGCHGRFSLSPQELASFKK-----ARDALBESLKLKNWSSPVPF 55
Db 6 LSPGVPVSRVLAAPSCPRG-----LLEECHTLEREILLIQRCLBEEYLR-----PCH 53

QY 56 PGNWDLRL-----LQVRPVPVLEAEALTLKVLAAAGPALEDVLDQPLHTLHILSOLA- 112
Db 54 PSEAALEPTLAEKEQKAMEQE-----LQASVGPSCV-----SPNHRQRLPGSSTOGL 102

QY 113 -----CTQPQTAGP--RPRGR--LHHWLHRLQEPKESA 144
Db 103 RPPLFCGVAPLQCCLPAPPLPYLRPGQSGATHRWGRLQCSPPREGPA 151

RESULT 14
US-08-061-636-2
; Sequence 2, Application US/08061636
; Patent No. 5858765
; GENERAL INFORMATION:
; APPLICANT: Myers, Alan M.
; APPLICANT: Maduale, Pascal
; TITLE OF INVENTION: Constitutive Pseudohyphal Growth Yeast
; TITLE OF INVENTION: Mutants
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:

; ADDRESS: Schwegman, Lundberg & Woessner
; STREET: 3500 IDS Center, 80 South Eighth Street
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
```

```
; ADDRESSEE: Merchant & Gould
; STREET: 3100 No. 5858765west Center
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402-4131
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/061.636
; FILING DATE: 12-MAY-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueeting, Ann M.
; REGISTRATION NUMBER: 33,977
; REFERENCE/DOCKET NUMBER: 9399.38-US01
; TELEPHONE: 612-332-5300
; TELEFAX: 612-332-9081
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 563 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-061-636-2

Query Match      8.4%; Score 80; DB 1; Length 563;
Best Local Similarity 23.5%; Pred. No. 3;
Matches 38; Conservative 20; Mismatches 44; Indels 60; Gaps 8;

QY 16 CHIGRFKSLSPQELASFKKARDALBESLKLKNWSSPVPFGNWLRLQLQVRPVALEA 75
Db 319 CHLGNK-----RDFVTDGFKLDIWSLGVTLY-----CLLYNELSPFGN 358

QY 76 ELALTLKVLAA-----GPALEDVL-----DQPLHTLHHI 106
Db 359 EFETHKILIEVLSKSKINGNTLNDLVIKRLLEKQVTLRISQDLVKVLSRDQPIDSRNH- 417

QY 107 LSQ-LQACIQPQTAGPRP--GRLLHHLHRLQEPKESAG 145
Db 418 -SQISSSVNPVRTEGPVRRPFGRL-----LTKGKKKTSG 452

RESULT 15
PCT-US94-05268-2
; Sequence 2, Application PC/TUS9405268
; GENERAL INFORMATION:
; APPLICANT: Iowa State University Research
; APPLICANT: Foundation, Inc.
; APPLICANT: Institut Pasteur
; APPLICANT: Institut National de la Sant et de la
; APPLICANT: Recherche M dicale
; APPLICANT: Myers, Alan M.
; APPLICANT: Maduale, Pascal
; TITLE OF INVENTION: Constitutive Pseudohyphal Growth Yeast
; TITLE OF INVENTION: Mutants
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESS: Schwegman, Lundberg & Woessner
; STREET: 3500 IDS Center, 80 South Eighth Street
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/05268
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/061,636
; FILING DATE: 12 MAY 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueing, Ann M. and Raasch, Kevin W.
; REGISTRATION NUMBER: 33,977 and 35,651
; REFERENCE/DOCKET NUMBER: 900.39WO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-339-0331
; TELEFAX: 612-339-3061
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 563 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US94-05268-2

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Query Match      8.4%; Score 80; DB 4; Length 563;
Best Local Similarity 23.5%; Pred. No. 3;
Matches 38; Conservative 20; Mismatches 44; Indels 60; Gaps 8;

Qy 16 CHIGRFKSLSPQELASFKKARDALFEESLKKNWSCSPVFFGNWDLRLQLQVRERPVALEA 75
Db 319 CHLGNK-----RDFVTDGFKLDIWSLGVTLY-----CLLYNELPFFGEN 358

Qy 76 ELALTLLKYLEAAA-----GPALEDVL-----DQPLHTLHHI 106
Db 359 EFETYHKIIEVSLSSKINGNTLNDLVIKRLLEKDVTLRISIQDLVKVLSRDQPIDSRNH- 417

Qy 107 LSQI-QACIQOPTAGPRPR--GRLLHWLRLQEPKESAG 145
Db 418 -SQISSSVNPNVTEGVPVRRPFGRL-----LTKGKKKKTSG 452

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Search completed: December 29, 2005, 14:00:44
Job time : 47 sec


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;
; CURRENT FILING DATE: 2004-08-09
; PRIOR APPLICATION NUMBER: US 60/493,194
; PRIOR FILING DATE: 2003-08-07
; PRIOR APPLICATION NUMBER: US 60/551,841
; PRIOR FILING DATE: 2004-03-10
; PRIOR APPLICATION NUMBER: US 60/559,142
; PRIOR FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 182
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: met IL-29 mutant C172X
; NAME/KEY: VARIANT
; LOCATION: (172)...(172)
; OTHER INFORMATION: Xaa = Ser, Ala, Thr, Val or Asn
US-10-914-772-41

Query Match          99.6%; Score 951; DB 5; Length 182;
Best Local Similarity 99.5%; Pred. No. 3.4e-86;
Matches 181; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MGPVPTSKPTTGGCHIGRFKSLSPQELASFKKARDALAEESLKLKNWCSVPVFGNWD 60
    |||||
Db 1 MGPVPTSKPTTGGCHIGRFKSLSPQELASFKKARDALAEESLKLKNWCSVPVFGNWD 60
    |||||
Qy 61 LRLQVRPVALEAEALTLKYLEAAAGPALEDVLDQPLHTLHHLSQLQACIQOPTA 120
    |||||
Db 61 LRLQVRPVALEAEALTLKYLEAAAGPALEDVLDQPLHTLHHLSQLQACIQOPTA 120
    |||||
Qy 121 GPRPRGLHHLRLQEAAPKESAGCLEASVTNLFRLTLRLKYVADGNLSLRTSTHPE 180
    |||||
Db 121 GPRPRGLHHLRLQEAAPKESAGCLEASVTNLFRLTLRLKYVADGNLSLRTSTHPE 180
    |||||
Qy 181 ST 182
    ||
Db 181 ST 182

RESULT 4
US-10-691-923-32
; Sequence 32, Application US/10691923
; Publication No. US20040138122A1
; GENERAL INFORMATION:
; APPLICANT: Klucher, Kevin M.
; APPLICANT: Sivakumar, Pallavur V.
; APPLICANT: Kindsvogel, Wayne R.
; APPLICANT: Henderson, Katherine E.
; TITLE OF INVENTION: METHODS FOR TREATING VIRAL INFECTION
; TITLE OF INVENTION: USING IL-28 AND IL-29
; FILE REFERENCE: 02-24
; CURRENT APPLICATION NUMBER: US/10/691,923
; CURRENT FILING DATE: 2003-10-23
; PRIOR APPLICATION NUMBER: US 60/420,714
; PRIOR FILING DATE: 2002-10-23
; PRIOR APPLICATION NUMBER: US 60/463,939
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: US 60/420,713
; PRIOR FILING DATE: 2002-10-23
; PRIOR APPLICATION NUMBER: US 60/463,982
; PRIOR FILING DATE: 2003-04-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 181
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: IL-29 mutant C171S
US-10-691-923-32

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Query Match 99.5%; Score 950; DB 4; Length 181;
Best Local Similarity 100.0%; Pred. No. 4.3e-86;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GVPVTSKPTTGGCHIGRFSLSPOELASFKKARDALLESLSLKNWSCSSPVFFGNWDL 61
DB 1 GVPVTSKPTTGGCHIGRFSLSPOELASFKKARDALLESLSLKNWSCSSPVFFGNWDL 60

QY 62 RLQVRRPVALEAEALTLKVLEAAAGPALEDVLDQPLHTLHHLSQLQACIQOPTAG 121
DB 61 RLQVRRPVALEAEALTLKVLEAAAGPALEDVLDQPLHTLHHLSQLQACIQOPTAG 120

QY 122 PRPRGLHHLRLQAPKESAGCLEASVTNLFRLTLRLKYVADGNLSLRTSTHPES 181
DB 121 PRPRGLHHLRLQAPKESAGCLEASVTNLFRLTLRLKYVADGNLSLRTSTHPES 180

QY 182 T 182
DB 181 T 181

RESULT 5

US-10-914-772-27
; Sequence 27, Application US/10914772
; Publication No. US20050037012A1
; GENERAL INFORMATION:
; APPLICANT: Brady, Lowell J.
; APPLICANT: Klucher, Kevin M.
; APPLICANT: Chan, Chung
; APPLICANT: Dong, Dennis L.
; APPLICANT: Liu, Hong Y.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Bukowski, Thomas R.
; TITLE OF INVENTION: HOMOGENEOUS PREPARATIONS OF IL-28 AND
; FILE REFERENCE: 03-10
; CURRENT APPLICATION NUMBER: US/10/914,772
; PRIOR FILING DATE: 2004-08-09
; PRIOR APPLICATION NUMBER: US 60/493,194
; PRIOR FILING DATE: 2003-08-07
; PRIOR APPLICATION NUMBER: US 60/551,841
; PRIOR FILING DATE: 2004-03-10
; PRIOR APPLICATION NUMBER: US 60/559,142
; PRIOR FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 181
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: IL-29 mutant C17S
US-10-914-772-27

Query Match 99.5%; Score 950; DB 5; Length 181;
Best Local Similarity 100.0%; Pred. No. 4.3e-86;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GVPVTSKPTTGGCHIGRFSLSPOELASFKKARDALLESLSLKNWSCSSPVFFGNWDL 61
DB 1 GVPVTSKPTTGGCHIGRFSLSPOELASFKKARDALLESLSLKNWSCSSPVFFGNWDL 60

QY 62 RLQVRRPVALEAEALTLKVLEAAAGPALEDVLDQPLHTLHHLSQLQACIQOPTAG 121
DB 61 RLQVRRPVALEAEALTLKVLEAAAGPALEDVLDQPLHTLHHLSQLQACIQOPTAG 120

QY 122 PRPRGLHHLRLQAPKESAGCLEASVTNLFRLTLRLKYVADGNLSLRTSTHPES 181
DB 121 PRPRGLHHLRLQAPKESAGCLEASVTNLFRLTLRLKYVADGNLSLRTSTHPES 180

QY 182 T 182

DB 181 T 181

RESULT 6

US-10-691-923-38
; Sequence 38, Application US/10691923
; Publication No. US20040138122A1
; GENERAL INFORMATION:
; APPLICANT: Klucher, Kevin M.
; APPLICANT: Sivakumar, Pallavur V.
; APPLICANT: Kindsvogel, Wayne R.
; APPLICANT: Henderson, Katherine E.
; TITLE OF INVENTION: METHODS FOR TREATING VIRAL INFECTION
; FILE REFERENCE: 02-24
; CURRENT APPLICATION NUMBER: US/10/691,923
; CURRENT FILING DATE: 2003-10-23
; PRIOR APPLICATION NUMBER: US 60/420,714
; PRIOR FILING DATE: 2002-10-23
; PRIOR APPLICATION NUMBER: US 60/463,939
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: US 60/420,713
; PRIOR FILING DATE: 2002-10-23
; PRIOR APPLICATION NUMBER: US 60/463,982
; PRIOR FILING DATE: 2003-04-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 182
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: met IL-29
US-10-691-923-38

Query Match 99.5%; Score 950; DB 4; Length 182;
Best Local Similarity 99.5%; Pred. No. 4.3e-86;
Matches 181; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MGPVPTSKPTTGGCHIGRFSLSPOELASFKKARDALLESLSLKNWSCSSPVFFGNWDM 60
DB 1 MGPVPTSKPTTGGCHIGRFSLSPOELASFKKARDALLESLSLKNWSCSSPVFFGNWDM 60

QY 61 LRLQVRRPVALEAEALTLKVLEAAAGPALEDVLDQPLHTLHHLSQLQACIQOPTA 120
DB 61 LRLQVRRPVALEAEALTLKVLEAAAGPALEDVLDQPLHTLHHLSQLQACIQOPTA 120

QY 121 GPRPRGLHHLRLQAPKESAGCLEASVTNLFRLTLRLKYVADGNLSLRTSTHPE 180
DB 121 GPRPRGLHHLRLQAPKESAGCLEASVTNLFRLTLRLKYVADGNLSLRTSTHPE 180

QY 181 ST 182
DB 181 ST 182

RESULT 7
US-10-914-772-15
; Sequence 15, Application US/10914772
; Publication No. US20050037012A1
; GENERAL INFORMATION:
; APPLICANT: Brady, Lowell J.
; APPLICANT: Klucher, Kevin M.
; APPLICANT: Chan, Chung
; APPLICANT: Dong, Dennis L.
; APPLICANT: Liu, Hong Y.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Bukowski, Thomas R.
; TITLE OF INVENTION: HOMOGENEOUS PREPARATIONS OF IL-28 AND
; FILE REFERENCE: 03-10
; CURRENT APPLICATION NUMBER: US/10/914,772
; CURRENT FILING DATE: 2004-08-09


```
; PRIOR APPLICATION NUMBER: US 60/493,194
; PRIOR FILING DATE: 2003-08-07
; PRIOR APPLICATION NUMBER: US 60/551,841
; PRIOR FILING DATE: 2004-03-10
; PRIOR APPLICATION NUMBER: US 60/559,142
; PRIOR FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 182
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: mature protein of SEQ ID NO: 3, with 3' Met added
US-10-914-772-15

Query Match      99.5%; Score 950; DB 5; Length 182;
Best Local Similarity 99.5%; Pred. No. 4.3e-86;
Matches 181; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MGPVPTSKPTTTGKGCHGRFKSLSPQELASFKKARDALAEESLKLKNWSCSPVPFGNWD 60
Db 1 MGPVPTSKPTTTGKGCHGRFKSLSPQELASFKKARDALAEESLKLKNWSCSPVPFGNWD 60

Qy 61 LRLQVRRPVALEAEALTLKVLAAAGPALEDVLDQPLHTLHLLSOLQACIQPQPTA 120
Db 61 LRLQVRRPVALEAEALTLKVLAAAGPALEDVLDQPLHTLHLLSOLQACIQPQPTA 120

Qy 121 GPRPRGLHHLRLQEQAPKESAGCLEASVTNLFRLLTRDLKYVADGNLSLRTSTHPE 180
Db 121 GPRPRGLHHLRLQEQAPKESAGCLEASVTNLFRLLTRDLKYVADGNLSLRTSTHPE 180

Qy 181 ST 182
Db 181 ST 182

RESULT 8
US-10-914-772-151
; Sequence 151, Application US/10914772
; Publication No. US20050037012A1
; GENERAL INFORMATION:
; APPLICANT: Brady, Lowell J.
; APPLICANT: Klucher, Kevin M.
; APPLICANT: Chan, Chung
; APPLICANT: Dong, Dennis L.
; APPLICANT: Liu, Hong Y.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Bukowski, Thomas R.
; TITLE OF INVENTION: HOMOGENEOUS PREPARATIONS OF IL-28 AND
; FILE REFERENCE: 03-10
; CURRENT APPLICATION NUMBER: US/10/914,772
; PRIOR FILING DATE: 2004-08-09
; PRIOR APPLICATION NUMBER: US 60/493,194
; PRIOR FILING DATE: 2003-08-07
; PRIOR APPLICATION NUMBER: US 60/551,841
; PRIOR FILING DATE: 2004-03-10
; PRIOR APPLICATION NUMBER: US 60/559,142
; PRIOR FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 151
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: IL-29 Leu insert after N-terminal Met, C173X
US-10-914-772-151

Query Match      99.5%; Score 950; DB 5; Length 182;
Best Local Similarity 99.5%; Pred. No. 4.3e-86;
Matches 181; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MGPVPTSKPTTTGKGCHGRFKSLSPQELASFKKARDALAEESLKLKNWSCSPVPFGNWD 60
Db 1 MGPVPTSKPTTTGKGCHGRFKSLSPQELASFKKARDALAEESLKLKNWSCSPVPFGNWD 60

Qy 61 LRLQVRRPVALEAEALTLKVLAAAGPALEDVLDQPLHTLHLLSOLQACIQPQPTA 120
Db 61 LRLQVRRPVALEAEALTLKVLAAAGPALEDVLDQPLHTLHLLSOLQACIQPQPTA 120

Qy 121 GPRPRGLHHLRLQEQAPKESAGCLEASVTNLFRLLTRDLKYVADGNLSLRTSTHPE 180
Db 121 GPRPRGLHHLRLQEQAPKESAGCLEASVTNLFRLLTRDLKYVADGNLSLRTSTHPE 180

Qy 181 ST 182
Db 181 ST 182

RESULT 8
US-10-914-772-151
; Sequence 151, Application US/10914772
; Publication No. US20050037012A1
; GENERAL INFORMATION:
; APPLICANT: Brady, Lowell J.
; APPLICANT: Klucher, Kevin M.
; APPLICANT: Chan, Chung
; APPLICANT: Dong, Dennis L.
; APPLICANT: Liu, Hong Y.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Bukowski, Thomas R.
; TITLE OF INVENTION: HOMOGENEOUS PREPARATIONS OF IL-28 AND
; FILE REFERENCE: 03-10
; CURRENT APPLICATION NUMBER: US/10/914,772
; PRIOR FILING DATE: 2004-08-09
; PRIOR APPLICATION NUMBER: US 60/493,194
; PRIOR FILING DATE: 2003-08-07
; PRIOR APPLICATION NUMBER: US 60/551,841
; PRIOR FILING DATE: 2004-03-10
; PRIOR APPLICATION NUMBER: US 60/559,142
; PRIOR FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 151
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: IL-29 Leu insert after N-terminal Met, C173X
US-10-914-772-151

Query Match      99.5%; Score 950; DB 5; Length 182;
Best Local Similarity 99.5%; Pred. No. 4.3e-86;
Matches 181; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MGPVPTSKPTTTGKGCHGRFKSLSPQELASFKKARDALAEESLKLKNWSCSPVPFGNWD 60
Db 1 MGPVPTSKPTTTGKGCHGRFKSLSPQELASFKKARDALAEESLKLKNWSCSPVPFGNWD 60

Qy 61 LRLQVRRPVALEAEALTLKVLAAAGPALEDVLDQPLHTLHLLSOLQACIQPQPTA 120
Db 61 LRLQVRRPVALEAEALTLKVLAAAGPALEDVLDQPLHTLHLLSOLQACIQPQPTA 120

Qy 121 GPRPRGLHHLRLQEQAPKESAGCLEASVTNLFRLLTRDLKYVADGNLSLRTSTHPE 180
Db 121 GPRPRGLHHLRLQEQAPKESAGCLEASVTNLFRLLTRDLKYVADGNLSLRTSTHPE 180

Qy 181 ST 182
Db 181 ST 182

RESULT 9
US-10-914-772-155
; Sequence 155, Application US/10914772
; Publication No. US20050037012A1
; GENERAL INFORMATION:
; APPLICANT: Brady, Lowell J.
; APPLICANT: Klucher, Kevin M.
; APPLICANT: Chan, Chung
; APPLICANT: Dong, Dennis L.
; APPLICANT: Liu, Hong Y.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Bukowski, Thomas R.
; TITLE OF INVENTION: HOMOGENEOUS PREPARATIONS OF IL-28 AND
; FILE REFERENCE: 03-10
; CURRENT APPLICATION NUMBER: US/10/914,772
; PRIOR FILING DATE: 2004-08-09
; PRIOR APPLICATION NUMBER: US 60/493,194
; PRIOR FILING DATE: 2003-08-07
; PRIOR APPLICATION NUMBER: US 60/551,841
; PRIOR FILING DATE: 2004-03-10
; PRIOR APPLICATION NUMBER: US 60/559,142
; PRIOR FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 155
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: IL-29 Ile insert after N-terminal Met, C173X
US-10-914-772-155

Query Match      99.2%; Score 947; DB 5; Length 183;
Best Local Similarity 98.9%; Pred. No. 8.6e-86;
Matches 180; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MGPVPTSKPTTTGKGCHGRFKSLSPQELASFKKARDALAEESLKLKNWSCSPVPFGNWD 60
Db 2 IGPVPTSKPTTTGKGCHGRFKSLSPQELASFKKARDALAEESLKLKNWSCSPVPFGNWD 61

Qy 61 LRLQVRRPVALEAEALTLKVLAAAGPALEDVLDQPLHTLHLLSOLQACIQPQPTA 120
Db 62 LRLQVRRPVALEAEALTLKVLAAAGPALEDVLDQPLHTLHLLSOLQACIQPQPTA 121

Qy 121 GPRPRGLHHLRLQEQAPKESAGCLEASVTNLFRLLTRDLKYVADGNLSLRTSTHPE 180
Db 121 GPRPRGLHHLRLQEQAPKESAGCLEASVTNLFRLLTRDLKYVADGNLSLRTSTHPE 180
```

Db 122 GPRPRGLHHLRLQAPKESAGCLESVTFNLFRLTRDLKYVADGNLXLTSTHPE 181
QY 181 ST 182
Db 182 ST 183

RESULT 10

US-10-914-772-40
; Sequence 40, Application US/10914772
; Publication No. US20050037012A1
; GENERAL INFORMATION:
; APPLICANT: Brady, Lowell J.
; APPLICANT: Klucher, Kevin M.
; APPLICANT: Chan, Chung
; APPLICANT: Dong, Dennis L.
; APPLICANT: Liu, Hong Y.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Bukowski, Thomas R.
; TITLE OF INVENTION: HOMOGENEOUS PREPARATIONS OF IL-28 AND
; FILE REFERENCE: IL-29
; FILE REFERENCE: 03-10
; CURRENT APPLICATION NUMBER: US/10/914,772
; PRIOR FILING DATE: 2004-08-09
; PRIOR APPLICATION NUMBER: US 60/493,194
; PRIOR FILING DATE: 2003-08-07
; PRIOR APPLICATION NUMBER: US 60/551,841
; PRIOR FILING DATE: 2004-03-10
; PRIOR APPLICATION NUMBER: US 60/559,142
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 40
; LENGTH: 181
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (171)...(171)
; OTHER INFORMATION: Xaa = Ser, Ala, Thr, Val or Asn

US-10-914-772-40

Query Match 99.1%; Score 946; DB 5; Length 181;
Best Local Similarity 99.4%; Pred. No. 1.le-85;
Matches 180; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 GVPVTSKPTTTGKGCHIGRFKSLSPQELASFKKARDALEESLKNWSCSSPVFPGNWDL 61
Db 1 GVPVTSKPTTTGKGCHIGRFKSLSPQELASFKKARDALEESLKNWSCSSPVFPGNWDL 60
QY 62 RLQVRRPVALAEALTLKYLEAAGPALEDVLDQPLHTLHLSQLQACIQPQTAG 121
Db 61 RLQVRRPVALAEALTLKYLEAAGPALEDVLDQPLHTLHLSQLQACIQPQTAG 120
QY 122 PRPRGLHHLRLQAPKESAGCLESVTFNLFRLTRDLKYVADGNLXLTSTHPE 181
Db 121 PRPRGLHHLRLQAPKESAGCLESVTFNLFRLTRDLKYVADGNLXLTSTHPE 180
QY 182 T 182
Db 181 T 181

RESULT 11

US-10-914-772-85
; Sequence 85, Application US/10914772
; Publication No. US20050037012A1
; GENERAL INFORMATION:
; APPLICANT: Brady, Lowell J.
; APPLICANT: Klucher, Kevin M.
; APPLICANT: Chan, Chung

; APPLICANT: Dong, Dennis L.
; APPLICANT: Liu, Hong Y.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Bukowski, Thomas R.
; TITLE OF INVENTION: HOMOGENEOUS PREPARATIONS OF IL-28 AND
; FILE REFERENCE: IL-29
; FILE REFERENCE: 03-10
; CURRENT APPLICATION NUMBER: US/10/914,772
; CURRENT FILING DATE: 2004-08-09
; PRIOR APPLICATION NUMBER: US 60/493,194
; PRIOR FILING DATE: 2003-08-07
; PRIOR APPLICATION NUMBER: US 60/551,841
; PRIOR FILING DATE: 2004-03-10
; PRIOR APPLICATION NUMBER: US 60/559,142
; PRIOR FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 85
; LENGTH: 182
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (172)...(172)
; OTHER INFORMATION: Xaa = Ser, Ala, Thr, Val, or Asn

US-10-914-772-85

Query Match 99.1%; Score 946; DB 5; Length 182;
Best Local Similarity 98.9%; Pred. No. 1.le-85;
Matches 180; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 MGPVPTSPTTTGKGCHIGRFKSLSPQELASFKKARDALEESLKNWSCSSPVFPGNWD 60
Db 1 MGPVPTSPTTTGKGCHIGRFKSLSPQELASFKKARDALEESLKNWSCSSPVFPGNWD 60
QY 61 LRLQVRRPVALAEALTLKYLEAAGPALEDVLDQPLHTLHLSQLQACIQPQPTA 120
Db 61 LRLQVRRPVALAEALTLKYLEAAGPALEDVLDQPLHTLHLSQLQACIQPQPTA 120
QY 121 GPRPRGLHHLRLQAPKESAGCLESVTFNLFRLTRDLKYVADGNLXLTSTHPE 180
Db 121 GPRPRGLHHLRLQAPKESAGCLESVTFNLFRLTRDLKYVADGNLXLTSTHPE 180
QY 181 ST 182
Db 181 ST 182

RESULT 12

US-10-914-772-161
; Sequence 161, Application US/10914772
; Publication No. US20050037012A1
; GENERAL INFORMATION:
; APPLICANT: Brady, Lowell J.
; APPLICANT: Klucher, Kevin M.
; APPLICANT: Chan, Chung
; APPLICANT: Dong, Dennis L.
; APPLICANT: Liu, Hong Y.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Bukowski, Thomas R.
; TITLE OF INVENTION: HOMOGENEOUS PREPARATIONS OF IL-28 AND
; FILE REFERENCE: IL-29
; FILE REFERENCE: 03-10
; CURRENT APPLICATION NUMBER: US/10/914,772
; CURRENT FILING DATE: 2004-08-09
; PRIOR APPLICATION NUMBER: US 60/493,194
; PRIOR FILING DATE: 2003-08-07
; PRIOR APPLICATION NUMBER: US 60/551,841
; PRIOR FILING DATE: 2004-03-10
; PRIOR APPLICATION NUMBER: US 60/559,142
; PRIOR FILING DATE: 2004-04-02

```

; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 161
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: IL-29 Glu, Ala, and Glu inserted after N-terminal
; OTHER INFORMATION: Met, C175X
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (175)...(175)
; OTHER INFORMATION: Xaa = Ser, Ala, Thr, Val, or Asn
US-10-914-772-161

Query Match      99.1%; Score 946; DB 5; Length 185;
Best Local Similarity 99.4%; Pred. No. 1.1e-85;
Matches 180; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  2 GVPVTSKPTTTGKGCHIGRFKSLSPQELASFKKARDALAEESLKLKNWSCSSPVFFGNWDL 61
Db  5 GVPVTSKPTTTGKGCHIGRFKSLSPQELASFKKARDALAEESLKLKNWSCSSPVFFGNWDL 64

QY  62 RLQVRRPVALEAEALTLKVLAAAGPALEDVLDQPLHTLHHLSQLQACIQOPTAG 121
Db  65 RLQVRRPVALEAEALTLKVLAAAGPALEDVLDQPLHTLHHLSQLQACIQOPTAG 124

QY  122 PRPRGRHLHWLRLQEAAPKESAGCLEASVTNLFRLTRDLKYVADGNLSLRTSTHPS 181
Db  125 PRPRGRHLHWLRLQEAAPKESAGCLEASVTNLFRLTRDLKYVADGNLSLRTSTHPS 184

QY  182 T 182
Db  185 T 185

RESULT 13
US-10-914-772-89
; Sequence 89, Application US/10914772
; Publication No. US20050037012A1
; GENERAL INFORMATION:
; APPLICANT: Brady, Lowell J.
; APPLICANT: Klucher, Kevin M.
; APPLICANT: Chan, Chung
; APPLICANT: Dong, Dennis L.
; APPLICANT: Liu, Hong Y.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Bukowski, Thomas R.
; TITLE OF INVENTION: HOMOGENEOUS PREPARATIONS OF IL-28 AND
; FILE REFERENCE: 03-10
; CURRENT APPLICATION NUMBER: US/10/914,772
; PRIOR FILING DATE: 2004-08-09
; PRIOR APPLICATION NUMBER: US 60/493,194
; PRIOR FILING DATE: 2003-08-07
; PRIOR APPLICATION NUMBER: US 60/551,841
; PRIOR FILING DATE: 2004-03-10
; PRIOR APPLICATION NUMBER: US 60/559,142
; PRIOR FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 89
; LENGTH: 182
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Met IL29 mutant T11P, Asn170, C172X
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (172)...(172)
; OTHER INFORMATION: Xaa = Ser, Ala, Thr, Val, or Asn
US-10-914-772-89
```

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Query Match      99.0%; Score 945; DB 5; Length 182;
Best Local Similarity 98.9%; Pred. No. 1.4e-85;
Matches 180; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY  1 MGPVTSKPTTTGKGCHIGRFKSLSPQELASFKKARDALAEESLKLKNWSCSSPVFFGNWDL 60
Db  1 MGPVTSKPTTTGKGCHIGRFKSLSPQELASFKKARDALAEESLKLKNWSCSSPVFFGNWDL 60

QY  61 LRLQVRRPVALEAEALTLKVLAAAGPALEDVLDQPLHTLHHLSQLQACIQOPTA 120
Db  61 LRLQVRRPVALEAEALTLKVLAAAGPALEDVLDQPLHTLHHLSQLQACIQOPTA 120

QY  121 GPRPRGRHLHWLRLQEAAPKESAGCLEASVTNLFRLTRDLKYVADGNLSLRTSTHPE 180
Db  121 GPRPRGRHLHWLRLQEAAPKESAGCLEASVTNLFRLTRDLKYVADGNLSLRTSTHPE 180

QY  181 ST 182
Db  181 ST 182

RESULT 14
US-09-895-834-5
; Sequence 5, Application US/09895834
; Publication No. US20020039763A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Preenell, Scott R.
; APPLICANT: Fox, Brian A.
; APPLICANT: Gilbert, Teresa
; APPLICANT: Haldeman, Betty A.
; APPLICANT: Grant, Francis J.
; TITLE OF INVENTION: INTERFERON-LIKE PROTEIN ZCYTO21
; FILE REFERENCE: 01-18
; CURRENT APPLICATION NUMBER: US/09/895,834
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 60/285,424
; PRIOR FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: 60/215,446
; PRIOR FILING DATE: 2000-06-30
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 200
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-895-834-5

Query Match      99.0%; Score 945; DB 3; Length 200;
Best Local Similarity 99.4%; Pred. No. 1.5e-85;
Matches 180; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  2 GVPVTSKPTTTGKGCHIGRFKSLSPQELASFKKARDALAEESLKLKNWSCSSPVFFGNWDL 61
Db  20 GVPVTSKPTTTGKGCHIGRFKSLSPQELASFKKARDALAEESLKLKNWSCSSPVFFGNWDL 79

QY  62 RLQVRRPVALEAEALTLKVLAAAGPALEDVLDQPLHTLHHLSQLQACIQOPTAG 121
Db  80 RLQVRRPVALEAEALTLKVLAAAGPALEDVLDQPLHTLHHLSQLQACIQOPTAG 139

QY  122 PRPRGRHLHWLRLQEAAPKESAGCLEASVTNLFRLTRDLKYVADGNLSLRTSTHPS 181
Db  140 PRPRGRHLHWLRLQEAAPKESAGCLEASVTNLFRLTRDLKYVADGNLSLRTSTHPS 199

QY  182 T 182
Db  200 T 200

RESULT 15
US-09-895-834-7
; Sequence 7, Application US/09895834
; Publication No. US20020039763A1
```

GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Fox, Brian A.
; APPLICANT: Gilbert, Teresa
; APPLICANT: Haldeman, Betty A.
; APPLICANT: Grant, Francis J.
; TITLE OF INVENTION: INTERFERON-LIKE PROTEIN ZCYTO21
; FILE REFERENCE: 01-18
; CURRENT APPLICATION NUMBER: US/09/895,834
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 60/285,424
; PRIOR FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: 60/215,446
; PRIOR FILING DATE: 2000-06-30
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 200
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-895-834-7

Query Match 99.0%; Score 945; DB 3; Length 200;
Best Local Similarity 99.4%; Pred. No. 1.5e-85;
Matches 180; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 GPVPTSKPTTGGCHIGRFKSLSPQELASFKKARDALAEESLKLKWSKSSPVPPGNWDL 61
DB 20 GPVPTSKPTTGGCHIGRFKSLSPQELASFKKARDALAEESLKLKWSKSSPVPPGNWDL 79
QY 62 RLQVREPVVAELALTLKVLAAAGPALEDVLDPLHTLHHLSQLQACIQOPTAG 121
DB 80 RLQVREPVVAELALTLKVLAAAGPALEDVLDPLHTLHHLSQLQACIQOPTAG 139
QY 122 PRPRGLHHLRLQAPKESAGCLEASVTNLFRLLTRDLKYVADGNLSLSTHPES 181
DB 140 PRPRGLHHLRLQAPKESAGCLEASVTNLFRLLTRDLKYVADGNLSLSTHPES 199
QY 182 T 182
DB 200 T 200

Search completed: December 29, 2005, 14:13:28
Job time : 165 secs